













## Fig. 4a

### Genomic sequence of the HtH1 gene

SIGNAL PEPTIDE SEQUENCE 1S-1 (1st part)

GGCTTGTTCAGTTTCTACTCGTCGCCCTTGTG

INTRON 1S-1/1S-2 (SEQ ID NO:109)

TTACAACCAACGTGTCTCTATTGGTCTTCACCTGTTTAACGTATATATTGTTTTTAATGT GAAAATCTGAGATTATTTCATTTCCGTCAATATTCGTAAAAATACTATACAAATAAAATT GCTTCAGCCTATTGCATTGGCAGTTTTCGCAGAATAACGAGGGAAGGCGTACATAAAATA TAAACCAGTGTATATTCAAGCATGTTTATAATTTCTTTATAGATTATAACATCATATCAA AACACCAATCTGGATTTAAACCCGTGAATCCAAAGTATACCAATTAACGGAACTTTATCA TGTTTTATCAAAGGTTTTAGATGAGGGTAAAGAAGTCCGAGCTATATTTTGCGATATCAG CAAAGCCTTCTATCACGTCTTGCACACAGGGCTGGTATCTAAACTCGAATCCACAGGAAT AAATATTTCAGCCGATAGAGAACAGTCGGTGGCTATCATTGGTCACAAAACAAGTCCAAA ATCTGCATTAGCCGGTGTTCCCCAAGGCTCTGTCTTGGGGCCCACTATTATTTCTCACCTA TATAAACGATTCAACTAATGGAATATAAAGCAACGTAAACCTCACCGCAGATGAAACACT AAGTTATAGACAATCCGTTTAAAACCCAGCCACTGCTTAATAATGACTTAGGCCGTCTTT CAGACTGGGCTAGTAAGCGGCAGGTTAAATTTCACCTTGAAAAGACAGAAACCATGGTAT ATTTCAAAAACACGAATGCAAGTCCTAAACTTCAACTACTACTTGATGATACTGGGATTT TGTTTTTTTCAATAACACGAATGCAAGTCCTAAACTTCAACTACTACTTGATGATACTG GGATTTCTAAAGTGTGTGGTGAACACAAACACCTTGGCCTGATTCTGCAAGATAATGGAA AATGTCAGAAACATAAGCAAGTTGATGTGGGGGTTTTCTGGGGGGTTGTGACAACACCGAAA GACCCTGCAACTAATGTTAGCTCAAAGGGTTTTACACCCGGTCACAAGTGGGGATCGACC CAGGCACCTTTTGCCTTTGACAGCTCGCCTTTCAAAAAATCTCAATTCGAAAACGAAATC TAATAATTTCATGAGCGATACAACCGTTTTTCATAATGCTGTGGTACCGCATACTGTGGA AACATCTGTCTACCCATTTGGTAGTCCCCCATAAAATGTATTTATGTTTATAAACACAAT GTTTATAGGGTTACAGTTAGAAGAAGCATTTCTATTGGCTAATGTACATTGCTTGTTTTT ACTATTGTGCAAAGGCATATTACAGGTCTTTTAGGAAATTAAATACTGTTTAAATCACAT ACACTACCGGTAATCCTATTATGCTTATCCTGCCAACATTCTGCCCAAGCAAACGCATGA AAGTTAAAGCTGAGTGTAAAATACTGATTGCTGTGTTACTTCACAACCAGTGGACTGAAT ACAACCATGTTTTTCTTGAAAGTCACAAACATCCAGTCGGTTTCTAATGTGTTAAGTTT GACTCCTAGTTCGTTACTTTTTTAATAAAACATCCATGTGTTTAATGTTTGGCCACAGAT ATAACAAGAAAGAAATCGGATAAAATCTACATTTTGACCAATCGGAAGGCTGCCCCCTCC CTAATCCTAATCATTTTTGTGCCTCAAAACATACTCAACCAGACATTTGAACTATGTATA TGCACAGACATGTGGTTGAGACACACTTGATTCAGTGCAGGATTATGTCCTTCAACCGAG TGTAGTCTTTAAGTGTGCCTGGAAACAAAAACTGCGTTGGGTTGCATCGCCTCTGTAGC AAGCTTGGACGCGTCACGCAGCTCTGATACCACGTATTGGCACCATGTTTCATCGGTCTC ACGCGAATATTATGCTATGTGTGGCGTATCATACCATAGGTTGGGAACGTTTCAATACTG TACCGAGCTTGGGCGTGTCACAAAGCTATGATAAGATGACAACACGTCTTGGCATCTTGT TTCCTCGGTATCACGCGCTGTTATGCTATGTGTGGCTATCACACCTTAGGTTGGGAAAGT

## Fig. 4b

TTCCACATTTTCCAGCCTCGTACATGTTTCCTTTTGTTTTTTCCTTAGTTATCAGCATACCGTATATTCTATATTTAATGAGCATTTGTATTTTTCTACAG

SIGNAL PEPTIDE SEQUENCE 1S-2(2nd part)

GTGGGGGCTGGAGCAG

INTRON 1S-2/1A-1 (SEQ ID NO:110)

GTGAGTTTCTTAACATTGTCATGGTACATGGATATACGCTCAGTGGGAAAGCAGGATATC CCCTTGGTTCAAGTATTCACTTGTCACGCCAAGTGTTCGATTCCCAACATGGAATACTGT CATATAGTAAATTGATACACTACTTACATTTAATTCTCCACTAAACGTCAACGTCCTTTA TAATGCTTATAAATATAAATTATATAAATACCTATAACTATAAATTAGTTATACTAGTAT TTATCAAAACATATTTGCCACGACACTGCACGCCGATACTTCAAGTGTCTTCACCTCAAG GCTTCATTAGTTTCGTCAGATGCGTGTATCCATACGAGTACATTCAGATTATGGGATCCA GAGACAGATGGCAACCGTTCTTTCCTCCTGACTAGGTGAGTGCCACTGATAAATCATTAT GCCTTTAACATTAGGAATGTTAGCAGTGCACATGTTTCAGAATTGCGACCTTATGGTTGT AAAGATTACAAACTTTACAACTTACTTGAGACAGGTTCCATATGTCGTATCTGAAATAGT GTGAAGGTATCTGATTCGATGCAATACACAGACATATAAACATATTGTCGCCCTGCTATT CCGGAAAGGTCATTTTGTATGTAACGTTCCTTAATGGACACAAACGGAATTATTAGTTAA ACATACTCAACAAAACTATGTTATTTTGCAATGGGTAGCACCGAAATCTACCGACAGTGG TTCGTAAAAGTAGAACATTCTGACATAAAGAAAAATCATTGGCTTTAAATATATGCAAGT TACTTGTCTCTAACAACCAGTTTTATACACATTTCAGAGAACGGGGAATCCGCGATGACA ATATCAACGAGTATATACAGAATATATAATTAAAAAACGATGAGTGCCTGGCAAGGGAAAG AGCGAGATTTGCCAAACAGGGGGGTGTTGTTGAGCTTGAATCGTGGAGAAACGTAGATTG AAAGACAAGATGACATCTAATGATCCGAAAATCAAACACAGGATTAACTGGGATGCAGAA GAATGAATATCTCAAGCATACATGCAACACTTCATGAATGCATCTCAAACATTTTCGTCA GATCGGATGCATGAAGATTTGTAAAGCAATGGTTTAAATTGTCCCTAAACGTTTAGTTGG AGATGTATGAGGCTAGGCTGTATGTTGAACGAAACCATTTAACATTGTTGTTCATGATTA TTTAATATTTTTCATTTTATAGATGTACAATAAAATTGGAAACTAAACATTTCCCTTTA TTGTTTTGTATTTACCTGTTCATGGGTATGTTTTGAAAGATCGTGATATTTAGTTGGCAT TCACAAGTTGGAAAAAGGTCACTCAGTTTGATTTCAAGTTTATGTAACCTCTTTATCTGA CGCTCCAAAATATGTATAGCCTTGTTCATCTGTCGGTATGTGGATATTCCTACTTCAGGG TAGGGTAGCATTAATACTTACAAAACATAACGTGTACCAGATTTCAGTCACCTCAGAGAT ACCCTGAATCGGAATGATACGTTACACTTTAGAAACAATTCACAAATATGACTGTCACCC TTTCAGGTAATAATGTTTGACGGACTACGATAGTGCTGAACAGCAGGAGAGGCAACATGG TTCGATTGTGAGACAGGTTTAGTGTATTTGTTTGCGAATTTAAGGTTCTGAATCACAATA GCTGGGATAAAGCTTAGTGGGACGTTAAGTCCCATCTCAATCTCTCACTTTTTTCCAAA ACAGTTTTAATTCAGGCTCATGACAAGGTCGTACTGTTGCAAAGGATTCTACTTCAAGCA GAGATGTCTCATGAATACAGTACAGGGTTTTTGAAGTTTATCCAGTGCAGCGCTGGCACC ATCTCTGCATGCGAATTATACCATCCATGCCGCTCTAGGCTATTTGTATTAAGTCTGTAG AATTAAATTCGCGAGTTGCAAATACTGCTCACCATTATCTGCCTCAACCCAGTTTGGGTA CATGCGATTTACACAATATTATGTATAATGTTCGCTTTTCGAAAACAAAACACCTAAATT CATCCAAAGTTTTGGGAGATTTTATTCGAGAAATCAACCTGAGATGTTGAATCGGGAGCT GCGCTTATTCAATGGTGGACTCGGAAGGGAAGTAACCGCTGATGAGGCAAAACAATAACG

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# Fig. 4c

TAATTTGACCATTCGAACAACTTTACTATTCTATTCATAATGTGTTTAGATTTACATTTG AATTAAAAGAGATGAGTTTAAGATATTAATATTTTCCTTTTATAGTCTGTCGTGATTGTA GGGCAATATTTATGTATGTTCGTTCATTTTTCATTTATCATTTGGAAAGGTATATCATAA TTCAATTTATTATCATCCGTCATCCAATTTTATTTCACGAAAGTATAAGAAATAACGAGA GAGAGAGAGAGAGAGAAAAGACAGAAATGAAGTTAGGAGATATNAGTTATCAAGAA AACAACAGTTTGAATTTTTTTTTTTAGACAAGATATCATATCAATAACCTCGCACTATTAC GGGAATAGGCGGGCGTTCCATATGCACAATGAATCGTCAGTTAAAATCAACATTAAACTT AAAATACTCCTCATATTTAAAGTTGATCTACCTCTTGTATTATTGTAGACTATTAGACAG AAGTCGACAGTGACACCAGCAACCAGATATCATACCCAGACTTAAAAAAGCTGTTTCCTTG ATGTTTCAATTTATTTCCATTTCCATTATTTCCCTTTATTGGTTTCCATTTATCAAACTT ATCAAGAATGTATAGGAGCTATTCCTTGTTCCTAAAACCGGATAGATCCATAATTTCCAT TTTGGGATAAATGGAAACTAAACACAACTTTTACAGTAAACACGAGTGAGCAAGTTGAGT TTTACGCCGTTTTTAGTAGTATTCCAGCAATATCGCGGCGGGGGACACCAGAAATGGGCT TCACACAGTGAATGCATGTGGGGATTCGAACCCGGGTCTTCGGCGTGACGAGTGAACGCT TTAGCCACTAGGCTACCCCACCGCCTATTTATAGTTAAGACGAATACTTTTCTCAAGCCT CAAATATGTCCATTCTAGAGAGACTGAATCTGATCCTGAATCTGCGGACCGGTCTTGAAT ATCATCCCACTAACTCATTGTACAAAGTACCTGTAGATTGTCAGTTCAAAGACAGATTTC TGATTTTAATCCTACTTTGAGATGTTTTAACTTTTATTCGATGCATTTTTTGCGTTCTGCG CGATCAGATTGAAACCGGAATGCACAGTGAAGTGTGGCATACATCTTTCCACAGAGATAC TGGATACTAGGTGGTACAACCGCATTGGCTTTGTGAAAGGATATTAGTGTTTTATGAGAC TGACTCATGTTTCAATGCTTAGAGCGGAATGATCTCGGTCTTCATGAAAAATATTGTGTT GAAGTAACCCCCCAGTCCCTAACAGAACGTGGGGAAAGCAGATGGATATGCCAAGACATC TTCGCATGGTGTGAAGATGATCGTTACAACATCTGCAGAAAAAGTTATTTCTGTGAAGAA TATGCCAAAGCATCACTGTGAGTGTTTTGAAGATGTGATATGGCAACACGCAGCGTGTAA TTATGCTTTGTGTGTATTTCTGAAGATCCGTATGAGCATGGCGCCCAAACTATCAGTTAAA TGGCTATGCGAAGATCTTCCCGAGATGGTAAACACATATTTTGGCCATTTTCTTTGTAAG TGGGCGACACAGAAGATCCCCCTGATTGTGTGGATGAGGACACAAAAACGGGTCCCCCTT CCACCAACCACAAGTTGTATAAATCGCTTGCGGACTTGAATACGGCAGTTGGACAGATAC ATACAGCCAGAGAGGGCCGAACTAAAACATCTAAACATGGAAAAACTGTAAAGACAGGCT TTGTTGTACGACGTACGTAAATTCATTGAATGTTTGAAAAGGTAGAAAATTATTAAATCT TTGAAACCTCGCTCTGTTTGTTTGTTATTGTCCCCCACATTTGCAAATGGTATCCAAAAA GGGCAGACACATTTGTTTTAATCTTAGCCAGGTTCAATTTAGCCTTGCGCCCCAGACTCAT TGTATCTGGTGAAGGCTATAGGTGGCCACGTCTTCTAAGATGCTATGCTATTCTTACCAG TCTCTCCTACCCAGAGTTCACCTGCACTGCTCCTGACTCACAATAAGCTGACGTGCTGTC ATATATGTGCAACATTGTATACGTTGGCGTTAAGCCCAACTCACTTCCGCTGTCTTTTGG CAG

DOMAIN 1A-1 (1st part of domain a)

ACAACGTCGTCAGAAAGGACGTGAGTCACCTCACAGTTGACGAGGTGCAAGCTCTTCACG GCGCCCTCCATGACGTCACTGCATCTACAGGGCCTCTGAGTTTCGAAGACATAACATCTT ACCATGCCGCACCAGCGTCGTGTGACTACAAGGGACGGAAGATCGCCTGCTGTGTCCACG GTATGCCCAGTTTCCCCTTCTGGCACAGGGCATATGTCGTCCAAGCCGAGCGGGCACTGT

## Fig. 4d

TGTCCAAACGGAAGACTGTCGGAATGCCTTACTGGGACTGGACGCAAACGCTGACTCACT TACCATCTCTTGTGACTGAACCCATCTACATTGACAGTAAAGGTGGAAAG

INTRON 1A-1/1A-2 (SEQ ID NO:111)

GTAACTACAAACGTCGTCCCATTCATACAGGAGAAATATACAATTGTGTTGTAAGAGCGG
TATACTGTTTGCCAACTGTGTAATTGAAACGTTGATGATGGTGTCTTTTGTATTTCAATTT
GTATGCACTTAGACATGATCAATGTTTCTGATGTGTCAAGGATGTTCGGTGTGTCACTTT
CAAAAGATCAAATTCATATGACGTACACAGAGCAAGAACCAACAGTAAGAAGTCTGTATG
ACTTCGCTCTTAAAAGCAATGGAAAAATATTTTCACTTAACACCTAGCCCATAATCACGC
ATATTAGATTATTCAAGCGATGTCAACATGTTTTTAATATCAATCTCATGGTTCTGATAT
TACCGGAGACATGCAACAGGCTGCCATTATAGCCAGGAAATCTTATGAATATGTGCATAT
TTTTTCTTTGATTCTGTATGACGAGAAATATTCGGAGGCAAAGATTGTGTTTTCAGAACA
GAATCAGGGTATCAGTGACATCGTCACTGCATGGCTACAATATTGCTGATGTGACTGTT
CTCCAAGGATTTTCATCTCACTGTCTGTACTTTGAATCTACAAATTCGTATTAAAGTTAT
GACAATTTTACCCCTGCCTATTTGTAAACGAAATATAACATGAGTGTTTTATGCTGACAG

DOMAIN 1A-2 (2nd part of domain a)

GCTCAAACCAACTACTGGTACCGCGGCGAGATAGCGTTCATCAATAAGAAGACTGCGCGA GCTGTAGATGATCGCCTATTCGAGAAGGTGGAGCCTGGTCACTACACACATCTTATGGAG ACTGTCCTCGACGCTCTCGAACAGGACGAATTCTGTAAATTTGAAATCCAGTTCGAGTTG GCTCATAATGCTATCCATTACTTGGTTGGCGGTAAATTTGA

INTRON 1A-2/1A-3 (SEQ ID NO:112)

GTAAGTTTGGTTTACAGTTTCATTATAAAAACATAGCAGTTTTAAGTTTAGGGGCCAGATT CTAATCTCTAATATTCCTTTCAACTCACTTTATTGGTGCCTTCTTGGAGTGACATTTAGA AACTAAGACAAGAGGAAGATGAACAATGTTTGTAGGGATAGACAGCTTGGATGCAATTTC GGACCAGATTCTAACAGCGTCATGAAGCAAGTGATACACAACGTTATCAATAACGAGAAT ATACACATAGATGGTTTGAGTTTATAAATGAACTATTAACGGCATTGTGGTTATAGACAG TGAGGAAGACGCCAGATAGACAAAGGGTAGGGGCCTTGGTTAGATAATGAGAAGTTGAAG AGGTGTAATAACTTAAATCTCTCTTGACTATTGATTGTGTCTAAGAGTTTTCTTATCTTA CAGTCGGCCAGTTGGGTCAAAGATGGTGTGATTCGGATGTGCTTTGTGTGTTCTGCGATG GCTGATTTAGAGTCAGTTTACTTCAGATGAATGAAGTTCCCCGATTCTTATGTTTAAGTT  ${\tt TGTTTCACCTACGCATGAAGACATCACCAGCAGGGTCGTCTTTATTTCTAGTAGCTTATT}$ TACAGCAAGCTTGTAACGTATGCTGAATTGCTGTGCCTCTGTAGAACACAGCATCTATGT GAATTGTTGACGTGGTGTTTGCCTTGATGGGTTCGTTGACTTGGTTTGTTGGATACTGA  ${\tt TTAAGGTGACTCTGCTGGGAGGCTTGGATTCTGGGGCCGGTGTTCTTTGCTCTCTGTCT}$ AGGGTGGCGATTATTTCCCAACCCACTTGTTCCATTACACTCAAAACCTGCTATCAATTT **ACAG** 

DOMAIN 1A-3 (3rd part of domain a)

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Fig. 4e

INTRON 1A-3/1A-4 (SEQ ID NO:113)

DOMAIN 1A-4 (4th part of domain a)

CTACGACAGCTTAAACCTGAATGGAATGACGCCAGAACAGCTGAAAACAGAACTAGACGA
ACGCCACTCCAAAGAACGTGCGTTTGCAAGCTTCCGACTCAGTGGCTTTGGGGGTTCTGC
CAACGTTGTTGTCTATGCATGTGTCCCTGATGATGATCCACGCAGTGATGACTACTGCGA
GAAAGCAGGCGACTTCTTCATTCTTGGGGGTCAAAGCGAAATGCCGTGGAGATTCTACAG
ACCCTTCTTCTATGATGTAACTGAAGCGGTACATCACCTTGGAGTCCCGCTAAGTGGCCA
CTACTATGTGAAAACAGAACTCTTCAGCGTGAATGGCACACCTTTCACCTGATCTTCT
TCCTCAACCAACTGTTGCCTACCGACCTGGGAAAGGTCACCTTGACC

INTRON 1A-4/1B (SEQ ID NO:114)

GTAAGTTGATTGTCTTAATATTGTTTTAATTTTTGCAGAAATTTGATTTTAAATTGTGTA AAAGGTTTCAATCGTGAAAACAAAAACAATTCTCTATCTGTATACCCCTCAATACCAGTA TGATCACAAATCTAGGAAATATTACAATACTGCTTCATAGAGTAACTGCTGTTTGTGGCA GAGCTGGATACGAAGTTTCTGATAGTTCACAGCTACATGATAGTAAATGAACCTGTACAC ATCAACGGTTGATCATGAAAATTTTGTATGTGTGAAAGTGCTACCTGTATTAGTGAACGT GCTACCTGTATAACTGAAAGTGCTACCTGTATGACTGAAAGTGCTACCTGTATGCTGAAA GTGCTACCTGTATTAGTGAACGTGCTACCTGTATAACTGAAAGTGCTACCTGTATGACTG AAAGTGCTACCTGTATTAGTGAAAGTGCTACCTGTATGAGTGAACGTGCTACCTGTATAA CTGAAAGTGCTACCTGTATGACTGAAAGTGCTACCTGTATTAGTGAAAGTGCTGCCTGTA TTAGTGAAAGTGCTACCTGTATGACTGAGCGTGTTACCTGTATGACTGAACGTGCTACCT GTATTAGTGAAAGTGTAATCTGTATGAGTGAAAGTGCTACCTGTATTAGTGAAAGTGCTA CTACCTGTGTGACTGAAAGTGCTACCTGTATTAGTGAAAGTGCTACCTGTATGACTGAAC GTGCTACCTGTATTAGTGATAGTGTCACTGGTACCAACTGGATGTTCTCACTTCTTTGGC GAATATCTGGGCTCAAAACAGTTTTTCAGTATCATAGTCGTATCAGTTTGATTTGTATGT GCAGTGGAATCATTTTCGTCAAATAATCAAAACTGGTGTTGAACTGGCGTTCACGTTTTA TGGTTGTAAAACAAATTCTGTAAGTAAAGATATTTTAGGGATATCTGTATGACATGAACT GAATTGCTTAAGGTTAGCATGCCATGACAAATTGCTGAATGTCTGAGGATTGGTGGAGCA ATAAATCATTATTAAGACAAAAATCAGAAACGTCCATTTTCACTTTTAACAGTGTATCTG TCTGAATGCCCCCTACTTTTTGGAAGAGTATATATGAATTATCGGCAATATAAAACGTTA AATGGCAAATGTCGGGCATATGTCAGGACATTATTACCGCAGTTTATAGTCATATTTACC GGGTCTAGGACAATTGTCACCCCGACAATTGCCACCCGGACAATTGCCACCCAAAAATAA AATATACGTAAACAGAAAACAAATATTGCTTTCAGCCTTTATTGAGTTAGATAATGACAT TTATGTTGATAAATATGTCGTTTGATAATAATAATAACAATAATATAATATTACAATACT 

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# Fig. 4f

ATGTTGTAGGCAACACTTCGTCGGTAGGCCGTTAGGTAGTTATCATTAGGGCTGAGTATT GCGCCAAATTTCGTATTGCTATATACTGCGATACACGGTTACCTGTTTTGCAATACGTAA ACTTAGGCAAATATGACAGTTTTTCCATGATTATTTTCACGTTTCAATGCTTAAAATGGT CTTATCTGTTATCTCCTTGAAGGTTTAATAAAATAACAATAAACATAAATCATTATTGAA GATTACTATCCAAGAATGTGAAATTCACAAACACCTTGGGATAACACTGCAAAACGACTG TTCATGGGACGGACATGAAAAAGGTGAGTCCCATGTTAAACTGTTGAGAAAGTTTCCTAT ATTACTGTTCTCATATTTGGGACAACTGTGCAGATCGGTAGCATCCAAGCTCGTCTAAAT CGGTTTGATAAACCTTGTCAAATAACATGTTGTCTCAACATCCAAGCTCACCTAAACCTT GTCAATACCTGCATCTGAACAAATGTATATTTAAGACGATAGCATCCAAGCTCATCTTTA AAATGAATATTTTCTCTTTTTCTACCAAAACATTATTTGGTTGACAGTTGTCCTCCCTAT TATAGTAAAAAGAACTGGGTGGCAATTGTCCTAGGTGGCAATTGTCCGGATGGCAATTGT CCGGGTGGCAATTGTCCGGGTGGCAGTTGTCCAGGTGGCTATTGTCCTGTTCCCATATTT ACGTATCCCATTTTCTGCTCTGTAATTTAAATAAACTCACCTGCCTAAGGTAAGACGAC ATGTGTCACGTGAACATCGTTTGGGGGCCAAGGGCGGAATCCCTTCGTTGAAAGTAAATGA ATACTGTACATAGAGATGCGTATCTTGAACTCTTTATTAGCTTTGATATTGTGCTTAATA TTTATTGCTTTATATGCTACATCAACATGTGTGTTTTCTTTTCATTTCAG

#### DOMAIN 1B

CACCTGTGCATCATCGCCACGATGACGATCTTATTGTTCGAAAAAATATAGATCATTTGA CTCGTGAAGAGGAATACGAGCTAAGGATGGCTCTGGAGAGATTCCAGGCCGACACATCCG TTGATGGGTACCAGGCTACAGTAGAGTACCATGGCCTTCCTGCTCGTTGTCCACGACCAG GGCTGTTCGTTACCCAGGTGGAAGATGCTCTTGTACGGCGTGGATCGCCTATCGGTGTTC CTTATTGGGACTGGACAAAACCTATGACTCACCTTCCAGACTTGGCATCAAATGAGACGT ACGTAGACCCGTATGGACATACACATCATAATCCATTCTTCAATGCAAATATATCTTTTG AGGAGGGACACCATCACACGAGCAGGATGATAGATTCGAAACTGTTTGCCCCAGTCGCTT TTGGGGAGCATTCCCATCTGTTTGATGGAATCCTGTACGCATTTGAGCAGGAAGATTTCT GCGACTTTGAGATTCAGTTTGAGTTAGTCCATAATTCTATTCATGCGTGGATAGGCGGTT CCGAAGATTACTCCATGGCCACCCTGCATTACACAGCCTTTGACCCCATTTTCTACCTTC ATCATTCCAATGTCGATCGTCTATGGGCAATCTGGCAAGCTCTTCAAATCAGGAGACACA AGCCATATCAAGCCCACTGTGCACAGTCTGTGGAACAGTTGCCAATGAAGCCATTTGCTT TCCCATCACCTCTTAACAACAACGAGAAGACACATAGTCATTCAGTCCCGACTGACATTT ATGACTACGAGGAAGTGCTGCACTACAGCTACGATGATCTAACGTTTGGTGGGATGAACC TTGAAGAATAGAAGAAGCTATACATCTCAGACAACAGCATGAACGAGTCTTCGCGGGAT ACCAACCACTCAAAGCTGGAGATATTGCCATTCTTGGTGGTGCCAAGGAAATGCCTTGGG CGTTTGACCGCTTGTATAAGGTCGAAATAACTGACTCATTGAAGACACTTTCTCTCGATG TCGATGGAGATTATGAAGTCACTTTTAAAATTCATGATATGCACGGAAACGCTCTTGATA CGGACCTGATTCCACACGCAGCAGTTGTTTCTGAGCCAGCTCACC

INTRON 1B/1C (SEQ ID NO:115)

GTAAGTAAATTTACAAAATTTGGTGTTCTCTAACTATCCTAAGTATTCAATCGTTAGCGT GTACCTATCTGCATAATGCAATACCCTGACTCCATATAAGTATAGTATATTTACTCTGGT CGAAAACAAACTTGAAAACAAGAGTGGACGTGCTGTTATGATTTCTTTTTCATTCTT GGTTCGTTGTGTAATGCCACAGCCAGCAATTCCAGATATATAGCGACGGTCTATGAATAC TCCAGTCTGGACCAGACAATCGTGTGGAATGGTTTAGGCACATTATATCAAATTCATTGT

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# Fig. 4g

#### DOMAIN 1C

CTACCTTTGAGGATGAAAAGCACAGCTTACGAATCAGAAAAAATGTCGACAGCTTGACTC CTGAAGAACAATGAACTGCGTAAAGCCCTGGAGCTTCTTGAAAATGATCATACTGCAG GTGGATTCAATCAGCTTGGCGCCTTCCATGGAGAGCCTAAATGGTGCCCTAATCCTGAAG CGGAGCACAAGGTTGCATGCTGTTTCATGGCATGGCTGTTTTCCCTCATTGGCACAGGC TTCTTGCTCTCCAGGCGGAGAATGCTCTTAGAAAGCATGGGTACAGTGGTGCTCTACCAT ACTGGGATTGGACTCGCCCCCTTTCCCAACTTCCTGATCTGGTTAGTCATGAGCAGTATA CAGATCCTTCCGACCATCACGTGAAGCATAACCCGTGGTTCAATGGCCACATCGATACAG TAAATCAGGATACCACCAGAAGCGTACGGGAGGATCTTTATCAACAACCTGAATTTGGAC ATTTCACGGATATTGCTCAACAAGTCCTCTTAGCATTAGAACAAGATGACTTCTGTTCGT TTGAAGTGCAGTATGAGATTTCCCATAATTTTATCCATGCACTTGTAGGAGGAACCGACG CTTATGGCATGGCATCGCTGAGATATACAGCATACGATCCAATCTTTTCTTGCATCATT CAAACACCGACAGGATCTGGGCTATTTGGCAATCCCTGCAAAAATACAGAGGCAAACCGT ACAACACTGCCAACTGCGCCATAGAATCTATGAGAAGGCCCCTGCAACCATTTGGACTAA GCAGTGCCATTAACCCTGACAGAATCACCAGAGAGCATGCTATCCCGTTTGATGTCTTCA ACTATAGAGATAACCTTCATTACGTATATGATACCCTGGAATTTAATGGTTTGTCGATTT CACAACTTGATAGAGAGCTGGAAAAAATCAAGAGTCACGAAAGAGTATTTGCTGGATTCT TGCTGTCGGGGGATTAAAAAATCTGCTCTTGTGAAATTCGAAGTTTGTACTCCACCTGATA ATTGTCATAAAGCAGGGGAGTTTTATCTACTCGGGGACGAAAACGAGATGGCTTGGGCCT ATGACCGACTTTTCAAGTATGATATTACTCAGGTTCTGGAAGCAAACCATCTACACTTCT ACCTGTTCCACACTGCAAATGTGGTACATGATTCCGGCACAG

INTRON 1C/1D (SEQ ID NO:116)

GTACGTGGATTGATTACATAGCAATGCTATATGATTTCAGTAATTACAACCTCAAGTCA
TGTAGCCGTTTTAGATTGCATTACATCAAACAGCATTGGATTAAATTGGGGGATTGTCCA
GGCCGCATTATGTTGCATTCCGAAAATAGTTTGTGTCCAGTGTCCACGTTTAAAATTAAA
CCATTTTAATCATATTAGGGATAATTTTAATAGATGTTATAGTGCTTTATTTCATATTGT
TACAGTGGACAGTCACCAAGGACATATTTTACTCTATAGATACACAAACACCAATTAAAA
CCCTGCTTTGGAAAGTCTAACTTTTTCCCCACAG

#### DOMAIN 1D

GCACCGTGATCGTGATAACTACGTTGAAGAAGTTACTGGGGCCAGTCATATCAGGAAGA
ATTTGAACGACCTCAATACCGGAGAAATGGAAAGCCTTAGAGCTGCTTTCCTGCATATTC
AGGACGACGGAACATATGAATCTATTGCCCAGTACCATGGCAAACCAGGCAAATGTCAAT
TGAATGATCATAATATTGCGTGTTGTGTCCATGGTATGCCTACCTTCCCCCAGTGGCACA
GACTGTATGTGGTTCAGGTGGAGAATGCTCTCCTAAACAGGGGATCTGGTGTGGCTGTTC
CTTACTGGGAGTGGACTGCTCCCATAGACCATCTACCTCATTTCATTGATGATGCAACAT
ACTTCAATTCCCGACAACAGCGGTACGACCCTAACCCTTTCTTCAGGGGAAAGGTTACTT
TTGAAAACGCAGTCACAACAAGGGACCCACAAGCCGGGCTCTTCAACTCAGATTATATGT
ATGAGAATGTTTTACTTGCACTGGAGCAGGAAAATTATTGTGACTTTGAAATTCAGTTTG
AGCTTGTTCATAACGCACTTCATTCCATGCTGGGAGGTAAAGGGCAGTACTCCATGTCCT

# Fig. 4h

INTRON 1D/1E (SEQ ID NO:117)

GTAATGCCATCTTAATACAGTTCGTTCGTTAAATTATATATGTTCGTTTACAACACCATA CCTTGAATTGAGGTAATACATCACTTGATATTGATAATGTAATGGTAATTGTTCTTGTTT GTAAAACCGTTTCTGGGGTGTTTATTCACTATCCACCTGGTGGATAGTGAGTAAAACACAT TCGGTTTAATATGGGTATCTAATGGACAGTGAAGTGTGCTGGCTAGGCAGATACCTTGGT TTCTGTGAATGGAGGTAGTAGAAAGGGGTTTTGATGATTGCAG

#### DOMAIN 1E

ATACCCATATCTTGGACCACGACCATGAGGAAGAGATACTTGTCAGGAAGAATATAATTG ATTTGAGCCCAAGGGAGAGGGTTTCTCTAGTCAAAGCTTTGCAAAGAATGAAGAATGATC GCTCCGCTGATGGGTACCAAGCCATTGCCTCTTTCCATGCCCTGCCACCACTCTGTCCCA ATCCATCTGCAGCTCACCGTTATGCTTGCTGTCCATGGCATGGCTACATTTCCCCAGT GGCACAGACTGTACACTGTTCAGGTTCAGGATGCCCTGAGGAGACATGGTTCACTTGTTG CAACATTTTATCATCCAATCCGGAATATTAATATTTCAAATCCATTCCTCGGGGCTGACA TAGAATTTGAAGGACCGGGCGTTCATACAGAGAGGCACATAAATACTGAGCGCCTGTTTC ACAGTGGGGATCATGACGGATACCACAACTGGTTCTTCGAAACTGTTCTCTTTGCTTTGG AACAGGAAGATTACTGCGATTTTGAAATACAATTTGAGATAGCCCATAATGGCATCCACA CATGGATTGGTGGAAGCGCAGTATATGGCATGGGACACCTTCACTATGCATCATATGATC CAATTTTCTACATCCACCATTCACAGACGGACAGAATATGGGCTATTTGGCAAGAGCTGC AGAAGTACAGGGGTCTATCTGGTTCGGAAGCAAACTGTGCCATTGAACATATGAGAACAC CCTTGAAGCCTTTCAGCTTTGGGCCACCCTACAATTTGAATAGTCATACGCAAGAATATT CAAAGCCTGAGGACACGTTTGACTATAAGAAGTTTGGATACAGATATGATAGTCTGGAAT TGGAGGGGCGATCAATTTCTCGCATTGATGAACTTATCCAGCAGAGACAGGAGAAAGACA GAACTTTTGCAGGGTTCCTCCTTAAAGGTTTTGGTACATCCGCATCTGTGTCATTGCAAG TTTGCAGAGTTGATCACACCTGTAAAGATGCGGGCTATTTCACTATTCTGGGAGGATCAG CCGAAATGCCATGGGCATTCGACAGGCTTTATAAGTATGACATTACTAAAACTCTTCACG ACATGAACCTGAGGCACGAGGACACTTTCTCTATAGACGTAACTATCACGTCTTACAATG GAACAGTACTCTCGGGAGACCTCATTCAGACGCCCTCCATTATATTTTGTACCTGGACGCC

INTRON 1E/1F-1 (SEQ ID NO:118)

GTGAGTACCTGTTTGCACTAAGACTTCTGTAGGCTAAAAGTGTAAGAAATATCAATTAAT TTCAATTCACCCAAACTTGAAAACGGTACCTATATAGGTTAACTTTTTGTCTACAGTAAA CTGAACATACCTACACATTTCATGAAATGATCTCTCAATATTTTCCACCAACAG

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Fig. 4i

DOMAIN 1F-1 (1st part of domain f)

ATAAACTCAACTCACGGAAACATACACCTAACAGAGTCCGCCATGAGCTAAGTAGCCTTA GTTCCCGTGACATAGCAAGCTTGAAGGCAGCTTTGACAAGCCTTCAACATGATAATGGGA CTGATGGTTATCAAGCTATTGCTGCCTTCCATGGCGTTCCTGCGCAGTGCCACGAGCCAT CTGGACGTGAG

INTRON 1F-1/1F-2 (SEQ ID NO:119)

DOMAIN 1F-2 (2nd part of domain f)

ATCGCCTGTTGCATCCACGGCATGGCGACGTTTCCTCACTGGCACCGGTTGTACACTCTG CAGTTGGAGCAAGCGCTGCGCAGACACGGGTCCAGTGTTGCTGTTCCATACTGGGACTGG ACCAAGCCAATCACCGAACTGCCACACATTCTGACAGACGGAGAATATTATGACGTTTGG CAAAATGCCGTCTTGGCCAATCCGTTTGCAAGAGGTTATGTGAAAATTAAAGATGCATTT ACGGTGAGAAATGTCCAGGAAAGTCTGTTCAAAATGTCAAGTTTTGGAAAGCACTCGCTT CTGTTTGACCAGGCTTTGTTGGCTCTTGAACAAACTGACTACTGTGACTTCGAAGTTCAG TTTGAAGTGATGCATAACACGATCCATTATCTCGTAGGAGGGCGTCAAACGTACGCCTTC TCCTCTCGAGTATTCCTCATACGATCCAATCTTCTTTATTCACCACTCGTTTGTTGAC AAAATATGGGCTGTATGGCAAGAACTGCAAAGCAGGAGACATCTACAGTTTAGAACAGCT GATTGTGCTGTGGGCCTCATGGGTCAGGCAATGAGGCCTTTCAACAAGGATTTCAACCAC AACTCGTTCACCAAGAAGCACGCAGTCCCTAATACAGTATTTGATTATGAAGATCTTGGC TATAACTATGACAACCTTGAAATCAGTGGTTTAAACTTAAATGAGATCGAGGCGTTAATA GCAAAACGCAAGTCACATGCTAGAGTCTTTGCTGGGTTCCTGTTGTTTGGATTAGGAACT TCGGCTGATATACATCTGGAAATTTGCAAGACATCGGAAAACTGCCATGATGCTGGTGTG ATTTTCATCCTTGGAGGTTCTGCAGAGATGCATTGGGCATACAACCGCCTCTACAAGTAT GACATTACAGAAGCATTGCAGGAATTTGACATCAACCCTGAAGATGTTTTCCATGCTGAT GAACCATTTTTCCTGAGGCTGTCGGTTGTTGCTGTGAATGGAACTGTCATTCCATCGTCT CATCTTCACCAGCCAACGATAATCTATGAACCAGGCGAAG

INTRON 1F-2/1G-1 (SEQ ID NO:120)

GTGAGATATATGCAAATTGAATGTTGTCCAGATGCGTTGTTTACATTTATATGCTTGGAA
TTGTCCTGAACGAATACAGTGGAATAACCAAAAGCTGAAAAATAAAAAGATATATACTTC
ATTCTGAATTTGTCAGTATTGCTGACCCAAAAACACGTTATCCATGTCGACACTATATTT
GCCTTTCTGAATCTGAGACTGCGTTATGTTTCTAATAATCACGAAATATGGTATACAGGT
TGTGTATCTGTAGAATACCCAAGGCAGAATTTAAAGGGTCACACCCTGTTTAATACAG

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Fig. 4j

DOMAIN 1G-1 (1st part of domain g)

ATCACCATGACGACCATCAGTCGGGAAGCATAGCAGGATCCGGGGTCCGCAAGGACGTGA ACACCTTGACTAAGGCTGAGACCGACAACCTGAGGGAGGCGCTGTGGGGTGTCATGGCAG ACCACGGTCCCAATGGCTTTCAAGCTATTGCTGCTTTCCATGGAAAACCAGCTTTGTGTC CCATGCCTGATGGCCACAACTACTCATGTTGTACTCACG

INTRON 1G-1/1G-2 (SEQ ID NO:121)

GTAAGTTTGTGTTGGTTAGTGTTGGTTGCATGTTTTGCCATATCGATAGTATCAGTGTGG TAACATCTGGTTTCTAGTTCAGTTCACCTTATCAGAAGCTGTTTGCTCTCGTCTAC AATAGTGACGTCTTTCAGTTTTAGAACCGTGTACATCCGGGTTATATTGGTCTCCAGCAA CCCGTGCTTGTCGTGGGAGGCCACTGATGGGAACGGGTGGTCAGACTCGCTCACTTAGTT GACACATGTCAATTGCGAAGATCGATGCTGAGGTTGTTAAACATTGGATTGTCTGGTCCA GACTCGATTATTTACAGACAGCCGCCATGTACCTGGAATATTGCTGAGTGCGGCGTTAAA CAACAAACTAGTCAGACTAATCTTTCACTGTTTATAATGATGGCTCGAACCTAGCACTCA TGTCCCAAGTTGGCGAACATCTGGAAGGGAATTTCAAATGAAAAGAACAATCTTTCACGT CTATTGGTATCACGCTCCTGGAGAAGAACATGATGTTCACGGCGTTACTTCCTCTTACCT GTTTTACTTGTTCCCACGTTTCTTCATATTTAAAGAGTATTTGGGTATTAGAGCTTTGGT GCTGTTACAATGCTACTCAACTGTTCAGTGCGGGCGACCGCGCTTGTTTACACATTAAGT TGTGTCTGTGTCTATGTGTGTGTCTGCGTGTGTCTGTGTCCGTATGTGGCTGTCTA TGTGTGTGTGTGTGTTTATGTGTGTATATGCGTGTGTGTCTGTGTCCGTATGTGGC TGTGTCTATGTGTGACATGCAATACATGCTGTGATACTCACTAGCTGCGTCTATCGAC CAG

DOMAIN 1G-2 (2nd part of domain g)

INTRON 1G-2/1G-3 (SEQ ID NO:122)

DOMAIN 1G-3 (3rd part of domain g)

GGACACATTGATTATCTCAATGTCAGCACAACTCGATCTCCCCGAGACATGCTGTTCAAC GACCCCGAGCATGGATCAGAGTCGTTCTTCTACAGACAAGTCCTCTTAGCTCTGGAACAA

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## Fig. 4k

INTRON 1G-3/1H (SEQ ID NO:123)

GTGAGTACGACAGGCATTTCTAGTAAAAACCTACTTTTGGTAAAAAGGTTCGAGAAATCAC
TTGAAGCAACAACATGATTTTGTAACGCCTATTACACGTGAACATGTCACACCCGGTGAT
GCCGTTTAATGGACATGCCTCTGTTAATGAAAGGGGTAAGTACATGTGTATGGGGATGGG
ATGGGAGCCACCTGTCCCAATTTCATAGGTCCCTAGGATCCCAGTTGCGTAGGAATCCCC
TGATTAATGCCTTGTGAATTCCTCCTGGAATTGTCCTGGCCCAAATTTTTACAAACCCGC
CCCGATATACCTTGGAAATAATTGGGCCTAAGGGTGGGGCTTTTAAGGACCAAGAACCCA
ACCTAAACCCCAACCCATTTTTCCCACCCATTCCAGGTTTTGTTTTACCAAATAAAAAG
GTTTCCACTTTGAGGAAACCCTTTAAGGGTTCTTTTCAGGGCTTTTTTTCTTTTCTGGGA
ATTCCAATTCCGGGGGAACAAAATACATATATTTCACAGACCTTTGGTCAAATTTATATA
ATTTCCGACTTCATGTCATAGGTTTTGTCTTTCCTACACAG

#### DOMAIN 1H

TGCACAGAGGCGGAAACCACGAAGATGAACACCATGATGACAGACTCGCAGATGTCCTGA TCAGGAAAGAAGTTGACTTCCTCTCCCTGCAAGAGGCCAACGCAATTAAGGATGCACTGT ACAAGCTCCAGAATGACGACAGTAAAGGGGGGCTTTGAGGCCCATAGCTGGCTATCACGGGT ATCCTAATATGTGTCCAGAAAGAGGTACCGACAAGTATCCCTGCTGTGTCCACGGAATGC CCGTGTTCCCCCACTGCACCGCCTGCATACCATTCAGATGGAGAGAGCTCTGAAAAACC ATGGCTCTCCAATGGGCATTCCTTACTGGGATTGGACAAAGAAGATGTCGAGTCTTCCAT CTTTCTTTGGAGATTCCAGCAACAACACCCTTTCTACAAATATTACATCCGGGGCGTGC AGCACGAAACAACCAGGGACATTAATCAGAGACTCTTTAATCAAACCAAGTTTGGTGAAT TTGATTACCTATATTACCTAACTCTGCAAGTCCTGGAGGAAAACTCGTACTGTGACTTTG AAGTTCAGTATGAGATCCTCCATAACGCCGTCCACTCCTGGCTTGGAGGAACTGGAAAGT ATTCCATGTCTACCCTGGAGCATTCGGCCTTTGACCCTGTCTTCATGATTCACCACTCGA GTTTGGATAGAATCTGGATCCTTTGGCAGAAGTTGCAAAAGATAAGAATGAAGCCTTACT ACGCATTGGATTGTGCTGGCGACAGACTTATGAAAGACCCCCTGCATCCCTTCAACTACG AAACCGTTAATGAAGATGAATTCACCCGCATCAACTCTTTCCCAAGCATACTGTTTGACC TTGAAGAGGTAATTCAGGAATTAAGAAACAAAGATCGCATATTTGCTGGTTTTGTTTTGT ACGAAGAATATGCAGGAGAATTTGCAGTTTTGGGAGGTGAGAAGGAGATGCCGTGGGCAT ATGAAAGAATGCTGAAATTGGACATCTCCGATGCTGTACACAAGCTTCACGTGAAAGATG AAGACATCCGTTTTAGAGTGGTTGTTACTGCCTACAACGGTGACGTTGTTACCACCAGGC TGTCTCAGCCATTCATCGTCCACCGTCCAGCCCATGTGGCTCACGACATCTTGGTAATCC CAGTAGGTGCGGCCATGACCTTCCGCCTAAAGTCGTAGTAAAGAGCGGCACCAAAGTCG

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# Fig. 41

AGTTTACACCAATAGATTCGTCGGTGAACAAAGCAATGGTGGAGCTGGGCAGCTATACTG CTATGGCTAAATGCATCGTTCCCCCTTTCTCTTACCACGGCTTTGAACTGGACAAAGTCT ACAGCGTCGATCACGGAGACTACTACATTGCTGCAGGTACCCACGCGTTGTGTGAGCAGA ACCTCAGGCTCCACATCCACGTGGAACACGAGTAG

3 UTR

**TTCACAG** 

INTRON 3'UTR (SEQ ID NO:124)

GTGAGGAGAGGCCCCAGGCTAGCAGGGCAATGGATGAAGGAAATAGGGGCAAAGGGAAT
AGCAGTTACACCATCGACATTTCCAACCTCCTCAGAAACTAATATATAGCCTTAATACAA
CCAGCCAAGACTCAACGGGCAGCCGGGGTGGGGGGATTTGGTGGTCGCTGTTTCAGACCA
GGGTGCAAAATATCAGTGCGCAAATCAACATGTTGCGTGTCAGACACTGACACAGCAGTC
ATTGAACCTGCAGACCCATAACAGGAAAATGGGGCAGATACGATCAAAGACAGTGTAAAA
TAGGGATAAGTAGGCATATGCAACCACCTGATGGAAATGAAAAGGGGTAAGTTTAAACCC
CGGCTACCAAAGGTCCAATGGTTCCTTAACCCAGCTTACGCTATCCCTCTAATTTCAGTA
TTGAGCTGATTTCTGTCGAGTTCATGTAAACTGTATACTTTCTGTATTATTACAG

3 UTR

## Fig. 5a

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### Primary structure of the HtH1 protein

SIGNAL PEPTIDE

LVQFLLVALVVGAGA

#### DOMAIN A

DNVVRKDVSHLTVDEVQALHGALHDVTASTGPLSFEDITSYHAAPASCDYKGRKIACCVHGMPSFP FWHRAYVVQAERALLSKRKTVGMPYWDWTQTLTHLPSLVTEPIYIDSKGGKAQTNYWYRGEIAFIN KKTARAVDDRLFEKVEPGHYTHLMETVLDALEQDEFCKFEIQFELAHNAIHYLVGGKFEYSMSNLE YTSYDPIFFLHHSNVDRLFAIWQRLQELRGKNPNAMDCAHELAHQQLQPFNRDSNPVQLTKDHSTP ADLFDYKQLGYSYDSLNLNGMTPEQLKTELDERHSKERAFASFRLSGFGGSANVVVYACVPDDDPR SDDYCEKAGDFFILGGQSEMPWRFYRPFFYDVTEAVHHLGVPLSGHYYVKTELFSVNGTALSPDLL PQPTVAYRPGK

#### DOMAIN B

GHLDPPVHHRHDDDLIVRKNIDHLTREEEYELRMALERFQADTSVDGYQATVEYHGLPARCPRPDA KVRFACCMHGMASFPHWHRLFVTQVEDALVRRGSPIGVPYWDWTKPMTHLPDLASNETYVDPYGHT HHNPFFNANISFEEGHHHTSRMIDSKLFAPVAFGEHSHLFDGILYAFEQEDFCDFEIQFELVHNSI HAWIGGSEDYSMATLHYTAFDPIFYLHHSNVDRLWAIWQALQIRRHKPYQAHCAQSVEQLPMKPFA FPSPLNNNEKTHSHSVPTDIYDYEEVLHYSYDDLTFGGMNLEEIEEAIHLRQQHERVFAGFLLAGI GTSALVDIFINKPGNQPLKAGDIAILGGAKEMPWAFDRLYKVEITDSLKTLSLDVDGDYEVTFKIH DMHGNALDTDLIPHAAVVSEPAH

#### DOMAIN C

PTFEDEKHSLRIRKNVDSLTPEETNELRKALELLENDHTAGGFNQLGAFHGEPKWCPNPEAEHKVA CCVHGMAVFPHWHRLLALQAENALRKHGYSGALPYWDWTRPLSQLPDLVSHEQYTDPSDHHVKHNP WFNGHIDTVNQDTTRSVREDLYQQPEFGHFTDIAQQVLLALEQDDFCSFEVQYEISHNFIHALVGG TDAYGMASLRYTAYDPIFFLHHSNTDRIWAIWQSLQKYRGKPYNTANCAIESMRRPLQPFGLSSAI NPDRITREHAIPFDVFNYRDNLHYVYDTLEFNGLSISQLDRELEKIKSHERVFAGFLLSGIKKSAL VKFEVCTPPDNCHKAGEFYLLGDENEMAWAYDRLFKYDITQVLEANHLHFYDHLFIRYEVFDLKGV SLGTDLFHTANVVHDSGT

#### DOMAIN D

GTRDRDNYVEEVTGASHIRKNLNDLNTGEMESLRAAFLHIQDDGTYESIAQYHGKPGKCQLNDHNI ACCVHGMPTFPQWHRLYVVQVENALLNRGSGVAVPYWEWTAPIDHLPHFIDDATYFNSRQQRYDPN PFFRGKVTFENAVTTRDPQAGLFNSDYMYENVLLALEQENYCDFEIQFELVHNALHSMLGGKGQYS MSSLDYSAFDPVFFLHHANTDRLWAIWQELQRFRELPYEEANCAINLMHQPLKPFSDPHENHDNVT LKYSKPQDGFDYQNHFGYKYDNLEFHHLSIPSLDATLKQRRNHDRVFAGFLLHNIGTSADITIYIC LPDGRRGNDCSHEAGTFYILGGETEMPFIFDRLYKFEITKPLQQLGVKLHGGVFELELEIKAYNGS YLDPHTFDPTIIFEPGT

#### DOMAIN E

DTHILDHDHEEEILVRKNIIDLSPRERVSLVKALQRMKNDRSADGYQAIASFHALPPLCPNPSAAH RYACCVHGMATFPQWHRLYTVQVQDALRRHGSLVGIPYWDWTKPVNELPELLSSATFYHPIRNINI SNPFLGADIEFEGPGVHTERHINTERLFHSGDHDGYHNWFFETVLFALEQEDYCDFEIQFEIAHNG

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### Fig. 5b

IHTWIGGSAVYGMGHLHYASYDPIFYIHHSQTDRIWAIWQELQKYRGLSGSEANCAIEHMRTPLKP FSFGPPYNLNSHTQEYSKPEDTFDYKKFGYRYDSLELEGRSISRIDELIQQRQEKDRTFAGFLLKG FGTSASVSLQVCRVDHTCKDAGYFTILGGSAEMPWAFDRLYKYDITKTLHDMNLRHEDTFSIDVTI TSYNGTVLSGDLIQTPSIIFVPGR

#### DOMAIN F

HKLNSRKHTPNRVRHELSSLSSRDIASLKAALTSLQHDNGTDGYQAIAAFHGVPAQCHEPSGREIA CCIHGMATFPHWHRLYTLQLEQALRRHGSSVAVPYWDWTKPITELPHILTDGEYYDVWQNAVLANP FARGYVKIKDAFTVRNVQESLFKMSSFGKHSLLFDQALLALEQTDYCDFEVQFEVMHNTIHYLVGG RQTYAFSSLEYSSYDPIFFIHHSFVDKIWAVWQELQSRRHLQFRTADCAVGLMGQAMRPFNKDFNH NSFTKKHAVPNTVFDYEDLGYNYDNLEISGLNLNEIEALIAKRKSHARVFAGFLLFGLGTSADIHL EICKTSENCHDAGVIFILGGSAEMHWAYNRLYKYDITEALQEFDINPEDVFHADEPFFLRLSVVAV NGTVIPSSHLHOPTIIYEPGE

#### DOMAIN G

DHHDDHQSGSIAGSGVRKDVNTLTKAETDNLREALWGVMADHGPNGFQAIAAFHGKPALCPMPDGH
NYSCCTHGMATFPHWHRLYTKQMEDAMRAHGSHVGLPYWDWTAAFTHLPTLVTDTDNNPFQHGHID
YLNVSTTRSPRDMLFNDPEHGSESFFYRQVLLALEQTDFCKFEVQFEITHNAIHSWTGGHSPYGMS
TLDFTAYDPLFWLHHSNTDRIWAVWQALQEYRGLPYNHANCEIQAMKTPLRPFSDDINHNPVTKAN
AKPLDVFEYNRLSFQYDNLIFHGYSIPELDRVLEERKEEDRIFAAFLLSGIKRSADVVFDICQPEH
ECVFAGTFAILGGELEMPWSFDRLFRYDITKVMKQLHLRHDSDFTFRVKIVGTDDHELPSDSVKAP
TIEFEPG

#### DOMAIN H

VHRGGNHEDEHHDDRLADVLIRKEVDFLSLQEANAIKDALYKLQNDDSKGGFEAIAGYHGYPNMCP ERGTDKYPCCVHGMPVFPHWHRLHTIQMERALKNHGSPMGIPYWDWTKKMSSLPSFFGDSSNNNPF YKYYIRGVQHETTRDINQRLFNQTKFGEFDYLYYLTLQVLEENSYCDFEVQYEILHNAVHSWLGGT GKYSMSTLEHSAFDPVFMIHHSSLDRIWILWQKLQKIRMKPYYALDCAGDRLMKDPLHPFNYETVN EDEFTRINSFPSILFDHYRFNYEYDNMRIRGQDIHELEEVIQELRNKDRIFAGFVLSGLRISATVK VFIHSKNDTSHEEYAGEFAVLGGEKEMPWAYERMLKLDISDAVHKLHVKDEDIRFRVVVTAYNGDV VTTRLSQPFIVHRPAHVAHDILVIPVGAGHDLPPKVVVKSGTKVEFTPIDSSVNKAMVELGSYTAM AKCIVPPFSYHGFELDKVYSVDHGDYYIAAGTHALCEQNLRLHIHVEHE

# Fig. 6a

### Genomic sequence of the HtH2 gene

DOMAIN 2A-1 (1st part of domain a) [domain a, parts 1-4: SEQ ID NO:156]

GGTCTTCCGTACTGGGACTGGACGCAGCATCTGACTCCAGATCTGGTGTCAGACCCCTTG TTTGTCGACCCGGAAGGAGGAAAG

INTRON 2A-1/2A-2 (SEQ ID NO:125)

CCGCCCTACTGGGGATCACAGGGAATGTATGTCAATGGTTGAAGAAAGGAGCAGTGGGTTACAACG CCGCGTTCAAAGTCATGGCAGTTTCATAGCGCATTGTGCGCGCGTGTGTATCTGTGTGCGCGCGTG TGTGCTTGCGTGCGTGTGAGTGAGTCCGCTTGTGCATTTGTACTAGCACAGACTAATGCTGGTTCT AGAGAGCCTACTGATAAATGTTTACATTAAGATCTTTACAGTATACTGAGATTCGAGCCCAGACCA GCGGAACACCAGGCAGGGTAACAACAAATAACGCCTTTCCACACAACCGACGCAGCCTAAAGTGGC TCTGATAGGCTGATACCGGTGTATTCTTAGAACTTGTAATTTGTGCTTTGCCATAATACATGTACT TCAGTTAACTGTAATACAGCATAAGACTGGACCGGTGTTTACGACGCAATGAGCAATAATTACTCT TCTCGTTTGTGTCAACGTATTCATAATCATTCTCATGCATCTGTTAGCTCAGATATTTTGATGTTT TACCTGGCGAGACAATAAGATCTTACTAGTGCTGCCACTTCAGTATGGTGTCCCCGATGGTGTCTG GTGTATGGGTGTGTTTGGCGTCAGTTGTTACTGGAAAAGTCAGCTCTAATTATGTCTTTATGTGGT TGACGCTTAAACGTTAGATGAATAAGGACTATATTGTGTTGTATAACATTTCTATAACCTCCTTTC TATATCATTTAG

DOMAIN 2A-2 (2nd part of domain a)

GCCCATGACAACGCATGGTATCGTGGAAACATCAAGTTTGAGAATAAGAAGACTGCAAGAGCTGTT GACGATCGCCTTTTCGAGAAGGTTGGACCAGGAGAGAATACCCGACTCTTTGAAGGAATTCTCGAT GCTCTTGAACAGGATGAATTCTGCAACTTCGAGATCCAGTTTGAGTTGGCTCACAACGCTATCCAC TACCTGGTTGGCGGCCGTCACAC

INTRON 2A-2/2A-3 (SEQ ID NO:126)

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Fig. 6b

DOMAIN 2A-3 (3rd part of domain a)

GTACTCCATGTCTCATCTCGAGTACACCTCCTACGACCCCCTCTTCTTCCTCCATCACTCCAACACCCGACCCGCATCTTCGCCATCTCGGCAACGTCTTCAGGTACTCAGAGGAAAGGACCCCAACACCCGCCGACTCCGCACACACCCCATGGAACCGTTCCGTCGGGACCTCGAACCCTCTTGACCTCACCAGGGAAAACTCCAAACCAATTGACAGCTTTGATTATGCCCACCTTGGCTACCA

INTRON 2A-3/2A-4 (SEQ ID NO:127)

DOMAIN 2A-4 (4th part of domain a)

GTATGATGACTTGACCCTGAACGGTATGACCCCAGAGGAATTGAACTCATATCTGCATGAACGGTC
AGGCAAGGAGGGGGGTGTTCGCAAGCTTCCGACTCTCAGGTTTTTGGCGGCTCTGCTAACGTTGTTGT
CTACGCATGCCGTCCTGCCCACGATGAAATGGCTGTCGATCAGTGCGACAAAGCCGGCGACTTCTT
TGTGTTGGGCGGACCCACCGAGATGCCCTGGAGGTTTTACAGAGCATTCCACTTCGACGTCACCGA
CAGCATCGACAACATCGACAAGGACCGCCACGGCCACTATTATGTAAAGGCGGAATTATTCAGTGT
AAATGGAAGTGCGCTACCGAATGATCTCCTGCCTCAACCCACCATCTCACACAGGCCAGCCCGCGG
ACACGTTGATG

INTRON 2A-4/2B (SEQ ID NO:128)

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# Fig. 6c

#### DOMAIN 2B

AGGAGGTGTACGAGCTGCGCAGAGCTATGGAGAGATTCCAGGCCGACACATCCGTTGATGGGTACC AGGCTACGGTTGAGTATCACGGCTTACCTGCTCGATGTCCATTCCCCGAGGCCACAAATAGGTTCG CCTGTTGCATCCACGGCATGGCGACATTCCCTCATTGGCACAGACTGTTCGTTACCCAGGTGGAAG ATGCACTGATCAGGCGAGGATCCCCTATAGGGGTCCCCTACTGGGACTGGACTCAGCCTATGGCAC ATCTCCCAGGACTTGCAGACAACGCCACCTATAGAGATCCCATCAGCGGAGACAGCAGACACAACC CGTTCCACGATGTTGAAGTTGCCTTTGAAAATGGGCGTACAGAACGTCACCCAGATAGTAGATTGT TTGAACAACCTCTATTTGGCAAACATACGCGTCTCTTCGACAGTATAGTCTATGCTTTTGAGCAGG AGGACTTCTGCGATTTTGAAGTTCAATTTGAGATGACCCATAATAATATTCACGCCTGGATTGGTG GCGGCGGAAGTATTCCATGTCTTCTACACTACACAGCCTTCGACCCTATCTCCTACCTTCATC AGGCTCATTGTGCTTGGTCTGAGGAACGCCAGCCTCTCAAACCTTTCGCCTTCAGTTCCCCACTGA ACAACAACGAAAAACCTACGAAAACTCGGTGCCCACCAACGTTTACGACTACGAAGGAGTCCTTG GCTATACTTATGATGACCTCAACTTCGGGGGCATGGACCTGGGTCAGCTTGAGGAATACATCCAGA GGCAGAGACAGAGACAGGACCTTTGCTGGCTTCTTTCTGTCACATATTGGTACATCAGCGAATG TTGAAATCATTATAGACCATGGGACTCTTCATACCTCCGTGGGCACGTTTGCTGTTCTTGGCGGAG AGAAGGAGATGAAATGGGGATTTGACCGTTTGTACAAATATGAGATTACAGATGAACTGAGGCAAC TTAATCTCCGTGCTGATGATGGTTTCAGCATCTCTGTTAAAGTAACTGATGTTGATGGCAGTGAGC 

INTRON 2B/2C (SEQ ID NO:129)

#### DOMAIN 2C

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# Fig. 6d

TTAAATTCTTTGTCTGCAAATCAGATGATGACTGTGACCACTATGCTGGTGAATTCTACATCCTTG GTGATGAAGCTGAAATGCCATGGGGCTATGATCGTCTTTACAAATATGAGATCACTGAGCAGCTCA ATGCCCTGGATCTACACATCGGAGATAGATTCTTCATCAGATACGAAGCGTTTGATCTTCATGGTA CAAGTCTTGGAAGCAACATCTTCCCCCAAACCTTCTGTCATACATGACGAAGGGGCAG

INTRON 2C/2D (SEQ ID NO:130)

GTGAGAACATTGATAATAGTTCAAATGAAGTATATCCGATTCAAGCTGTCGATACAAGATGAGATA CATAATCACAATGTTTGTATTAGATATCTCTCTTAATTTAATGCCGCTTTTATCAATATTCGAGCA ATCCTTCAGCAACATACACCAGCAAATGTTTCATCAACAGACTATATTATTTAATATTTTAAAAAT CCTTCTCTGTTGTTATAAATACTTAAAGTATCGAATTCCTTGAATGCGTCTTCTCTGCAGCATATA GTTAAGTTGTTGTGTTTCTCTGTCAG

#### DOMAIN 2D

AAGATCTGTCAAAGGGAGAAGTAGAGGCCTAAGGTCTGCCTTCCTGCAACTTCAGAACGACGGAG TCTATGAGAATATTGCCAAATTCCACGGCAAGCCTGGGTTGTGTGATGATAACGGTCGCAAGGTTG CCTGTTGTGTCCATGGAATGCCCACCTTCCCCCAGTGGCACAGACTCTATGTCCTCCAGGTGGAGA ATGCTTTGCTGGAGAGAGGATCTGCCGTCTCTGTGCCATACTGGGACTGGACTGAAACATTTACAG AGCTGCCATCTTTGATTGCTGAGGCTACCTATTTCAATTCCCGTCAACAAACGTTTGACCCTAATC CTTTCTTCAGAGGTAAAATCAGTTTTGAGAATGCTGTTACAACACGTGATCCCCAGCCTGAGCTGT ACGTTAACAGGTACTACCAAAACGTCATGTTGGCTTTTGAACAGGACAACTACTGCGACTTCG AGATACAGTTTGAGATGGTTCACAATGTTCTCCATGCTTGGCTTGGTGGAAGAGCTACTTATTCTA TGTGGGCCATCTGGCAGGAGCTGCAGAGGTACAGGAAGAAGCCATACAATGAAGCGGATTGTGCCA TTAACCTAATGCGCAAACCTCTACATCCCTTCGACAACAGTGATCTCAATCATGATCCTGTAACCT TTAAATACTCAAAACCCACTGATGGCTTTGACTACCAGAACAACTTTGGATACAAGTATGACAACC TTGAGTTCAATCATTTCAGTATTCCCAGGCTTGAAGAAATCATTCGTATTAGACAACGTCAAGATC GTGTGTTTGCAGGATTCCTCCTTCACAACATTGGGACATCCGCAACTGTTGAGATATTCGTCTGTG TCCCTACCACCAGCGGTGAGCAAAACTGTGAAAACAAAGCCGGAACATTTGCCGTACTCGGAGGAG AAACAGAGATGGCGTTTCATTTTGACAGACTCTACAGGTTTGACATCAGTGAAACACTGAGGGACC TCGGCATACAGCTGGACAGCCATGACTTTGACCTCAGCATCAAGATTCAAGGAGTAAATGGATCCT ACCTTGATCCACACATCCTGCCAGAGCCATCCTTGATTTTTGTGCCTGGTTCAA

INTRON 2D/2E (SEQ ID NO:131)

GTAAGAAAGTTTCACTGTCTAAATCTTTTTTTATGATAGAGGGGTAGAGAAGTGGAGACAATGTGAC AATATATTGAATAAAGTTGTTTAAAATTTATAACTCTCATAAGTTCATATTATGCTGAAGCTGTAG CCATCTATAACTGTGTAACATGAAATGTTAAGACATTAACCTAAATACTTCAGCTGATAACAAAAC AATGTTAATACATACGTCAATGTAACATTTCTTTATCTTTAGGTTATAGCATAAACACTTCAGAGA TACAGTGACGAAAACCTCTATTTAAATATTTCAG

#### DOMAIN 2E

GTTCTTTCCTGCGTCCTGATGGGCATTCAGATGACATCCTTGTGAGAAAAGAAGTGAACAGCCTGA CAACCAGGGAGACTGCATCTCTGATCCATGCTCTGAAAAGTATGCAGGAAGACCATTCACCTGATG GGTTCCAAGCCATTGCCTCTTTCCATGCCCTGCCACCACTCTGCCCTTCACCATCTGCAACTCACC GTTATGCTTGCTGTGTCCACGGCATGGCTACATTTCCCCAGTGGCACAGACTGTACACTGTACAGT

# Fig. 6e

TCCAGGATGCACTGAGGAGACATGGAGCTGCAGTAGGTGTACCGTATTGGGATTGGCTGCGACCGC AGTCTCACCTACCAGAGCTTGTCACCATGGAGACATACCATGATATTTGGAGTAACAGAGATTTCC TTGCAGACAAACTTTTTGTCAAAGGTGGACACGTTTTTGATAACTGGTTCTTCAAACAAGCCATCC TAGCGCTTGAGCAGGAAAACTACTGTGACTTTGAGATTCAGTTTGAAATTCTTCACAACGGCGTTC ACACGTGGGTCGGAGGCAGTCGTACCCACTCTATCGGACATCTCCATTACGCATCCTACGACCCTC TTTTCTACCTCCACCATTCCCAGACAGACCGTATTTGGGCAATCTGGCAAGAACTCCAGGAACAGA GAGGGCTCTCAGGTGATGAGGCTCACTGTGCTCTCGAGCAAATGAGAGAACCATTGAAGCCTTTCA GCTTCGGCGCTCCTTATAACTTGAATCAGCTAACACAGGATTTCTCCCGACCCGAGGACACCTTCG ACTACAGGAAGTTTGGTTATGAATATGACAATTTAGAATTCCTAGGAATGTCAGTTGCTGAACTGG ATCAATACATTATTGAACATCAAGAAAATGATAGAGTATTCGCTGGGTTCCTGTTGAGTGGATTCG GAGGTTCCGCATCAGTTAATTTCCAGGTTTGTAGAGCTGATTCCACATGTCAGGATGCTGGGTACT TCACCGTTCTTGGTGGCAGTGCTGAGATGGCGTGGGCATTTGACAGGCTATACAAATATGACATTA CTGAAACTCTGGAGAAAATGCACCTTCGATATGATGATGACTTCACAATCTCTGTCAGTCTGACCG CCAACAACGGAACTGTCCTGAGCAGCAGTCTAATCCCAACACCGAGTGTCATATTCCAGCGGGGAC ATC

INTRON 2E/2F-1 (SEQ ID NO:132)

GTAAGTAGTAAACTGCTCAGATTGTTTTCATAATTACTCCACTATTAAGTAAAAAGTACTAGTAAT TCAATAGTACTGTTCACAGAGAAATGTAACACAATAGACCACAGAGTCCATTTGTTAAACGCCTTT GGCTTGGTAAGTCTGAGATTTTGGTGACTGATGGAAAGCTAAAATATATTTTTGACAG

DOMAIN 2F-1 (1st part of domain f)

INTRON 2F-1/2F-2 (SEQ ID NO:133)

DOMAIN 2F-2 (2nd part of domain f)

ATCGCATGTTGCATTCACGGTATGCCGACCTTCCCCCAGTGGCACAGACTGTACACCCTGCAGTTGGAGATGGCTCTGAGGAGACATGGATCATCTGTCGCCATCCCCTACTGGGACCAAAGCCTATC

Nucleic Acid Molecule Comprising A Nucleic Acid Sequence Which Codes For A Haemocyanin And Comprising At Least One Intron Sequence (Serial No. 10/049,988; Inventor: Markl Jurgen)

### Fig. 6f

TCCGAACTCCCTCGCTCTTCACCAGCCCTGAGTATTATGACCCATGGCATGATGCTGTGGTAAAC
AACCCATTCTCCAAAGGTTTTGTCAAATTTGCAAATACCTACACAGTAAGAGACCCACAGGAGATG
CTGTTCCAGCTTTGTGAACATGGAGAGTCAATCCTCTATGAGCAAACTCTTCTTGCTCTAGAGCAA
ACCGACTACTGTGATTTTGAGGTACAGTTTGAGGTCCTCCATAACGTGATCCACTACCTTGTTGGC
GGACGTCAGACCTACGCATTGTCTTCTCTGCATTATGCATCCTACGACCCATTCTTCTTTATACAC
CATTCCTTTGTGGATAAGATGTGGGTAGTATGGCAAGCTCTTCAAAAGAGGGAGAAACTTCCATAC
AAGCGAGCTGACTGTCTCTAACCTAATGACTAAACCAATGAGGCCATTTGACTCCGATATGAAT
CAGAACCCATTCACAAAGATGCACGCAGTTCCCAACACACTCTATGACTACGAGAACCTGTACTAC
AGCTACGATAATCTCGAAAATAGGTGGCAGGAATCTCGACCAGCTTCAGGCTGAAATTGACAGAAGC
AGAAGCCACGATCGCGTTTTTGCTGGATTCTTGCTTCGTGGAATCGGAACTTCTTGCTGATGTCAGG
TTTTGGATTTGTAGAAATGAAAATGACTGCCACAGGGTGGAATAATTTTCATCTTAGGTGGAGCC
AAGGAAATGCCATGGTCATTTGACAGAAACTTCAAGTTTGATATCACCCATGTACTCGAGAAAGCT
GGCATTAGCCCAGAGGACGTGTTTGATGCTGAGGAGCCATTTTATATCAAGGTTGAGATCCATGCT
GTTAACAAGACCATGATACCATCGTCTGTGATCCCAGCCCCAACTATCATCTATTCTCCTGGGGAA

INTRON 2F-2/2G-1 (SEQ ID NO:134)

DOMAIN 2G-1 (1st part of domain g)

INTRON 2G-1/2G-2 (SEQ ID NO:135)

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# Fig. 6g

GGGCAGTGTAAGTAGCAACATTGTATATTAAATCAGTATATCGTACTTCAAAACACCAGGATTATG GGGTATACAGTGGGCAGTGTAAGTAGTAGCATTGTATATTAAATCAGTATATCGTACTTCAAAACA CCAGGATATAATTCAGTATATCGTGCTTCAAAACACCAGGATATAATTCAGTATATCGTGCTTCAA AACACCAGGATATATGGGATATACAGTGCGGGTTTGCATACAACCTCCACCCTTTACAG

DOMAIN 2G-2 (2nd part of domain g)

GTATGGCCTCCTTCCCACACTGGCACAGACTGTATGTGAAGCAGATGGAAGACGCCCTGGCTGACCACGATCACATATCGGCATCCCTTACTGGGACTGGACAACTGCCTTCACAGAGTTACCCGCCCTTGTCACAGACTCCGAGAACAATCCCTTCCATGAG

INTRON 2G-2/2G-3 (SEQ ID NO:136)

DOMAIN G-3 (3rd part of domain g)

INTRON 2G-3/2H (SEQ ID NO:137)

GTATGTTATCTTATTATCAAATGTGTAATCAGATACTGGAGACGTTTTCATATTAACTTGGTCAGC
ATTAGTTGATGATGTTTTGGTGCGATATTGACGACAAGGAGTTAAGCATTAACACGTTCAACACATCT
TTAATCTGATATGAGAAGGGAATAAATTGATCCAGTATTGATGATTGAAGTTAGATTAACAGTGAA
AGATATACCAGTTTTGATAATCGTATAAAACAGTAGCAGAATTGTATCGTGAAAACTAAATGTGGG
AAGGCGAACGCCAAGCAGATTTTAGATTACGATCGTGTGCTAGAATAATTCACAATAACCCAGACG
TCGGAAATGTGGTTGTCTATGGCAATAGTTACGATTAATTGCTAACATGCACGATTTACCTATTTC
AG

DOMAIN 2H

CCCACAGAGGACCAGTTGAAGAAACAGAAGTCACTCACCAAAATACTGACGGCAATGCACACTTCC ATCGTAAGGAAGTTGATTCGCTGTCCCTGGATGAAGCAAACAACTTGAAGAATGCCCTTTACAAGC

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## Fig. 6h

TACAGAACGACCACAGTCTAACAGGATACGAAGCAATCTCTGGTTACCATGGATACCCGAATCTGT GTCCGGAAGAAGGCGATGACAAATACCCCTGCTGCGTCCACGGAATGGCCATCTTCCCCCACTGGC ACAGACTCTTGACCATCCAACTGGAAAGAGCTCTCGAGCACAATGGTGCACTGCTTGGTGTTCCTT ACTGGGACTGGACCAAGGACCTGTCGTCACTGCCGGCGTTCTTCTCCGACTCCAGCAACAACAATC CCTACTTCAAGTACCACATCGCAGGTGTTGGTCACGACACCGTCAGAGAGCCCAACTAGTCTTATAT ATAACCAGCCCCAAATCCATGGTTATGATTATCTCTATTACCTAGCATTGACCACGCTTGAAGAAA ACAATTACTGTGACTTTGAGGTTCAGTATGAGATCCTCCACAACGCCGTCCACTCCTGGCTTGGAG GATCCCAGAAGTATTCCATGTCTACCCTGGAGTATTCGGCCTTTGACCCTGTCTTTATGATCCTTC ACTCGGGTCTAGACAGACTTTGGATCATCTGGCAAGAACTTCAGAAGATCAGGAGAAAGCCCTACA ACTTCGCTAAATGTGCTTATCATATGATGGAAGAGCCACTGGCGCCCTTCAGCTATCCATCTATCA ACCAGGACGAGTTCACCCGTGCCAACTCCAAGCCTTCTACAGTTTTTGACAGCCATAAGTTCGGCT ACCATTACGATAACCTGAATGTTAGAGGTCACAGCATCCAAGAACTCAACACAATCATCAATGACT AGATCTATCTCCGAACAGATGACAATGACGAAGAAGTTGGAACTTTCACTGTCCTGGGAGGAGAGA GGGAAATGCCATGGGCCTACGAGCGAGTTTTCAAGTATGACATCACAGAGGTTGCAGATAGACTTA AACTAAGTTATGGGGACACCTTTAACTTCCGACTAGAGATCACATCCTACGATGGATCGGTGGTAA ACAAGAGCCTACCCAATCCTTTCATCATCTACAGACCTGCCAATCATGACTACGATGTTCTTGTTA TCCCAGTAGGAAGAACCTTCACATCCCTCCCAAAGTTGTCGTCAAGAGAGGCACCCGCATCGAGT TCCACCCAGTCGATGATTCAGTTACGAGACCAGTTGTTGATCTTGGAAGCTACACTGCACTCTTCA ACTGTGTGGTACCACCGTTCACATACCGCGGATTCGAACTGAACCACGTCTATTCTGTCAAGCCTG GTGACTACTATGTTACCGGACCAACGAGAGACCTTTGCCAGAATGCAGATGTCAGGATTCATATCC ATGTTGAGGATGAGTAA

3 UTR

CGCAACAG

INTRON 3'UTR (SEQ ID NO:138)

3 UTR

GTTTCTTGGTCTCCACATATTCACACATCAGCACCAAACGGTTTCGAAGGACATTGGCGTTCTTCT CTGGCAATGCATTTCAATACAACATTGAAAATGACTTCAGCATATCAGTGTGCTTCGAACGTGTTC CGGAAGTACTCAAATGTGCTATGACTGAATTATTGTACATAACATAACTTATTGATGTTCAATAAAT AAATGTTGAAACG

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# Fig. 7a

### Primary structure of the HtH2 protein

#### DOMAIN A (SEQ ID NO:156)

GLPYWDWTQHLTQLPDLVSDPLFVDPEGGKAHDNAWYRGNIKFENKKTARAVDDRLFEKVGPGENT RLFEGILDALEQDEFCNFEIQFELAHNAIHYLVGGRHTYSMSHLEYTSYDPLFFLHHSNTDRIFAI WQRLQVLRGKDPNTADCAHNLIHEPMEPFRRDSNPLDLTRENSKPIDSFDYAHLGYQYDDLTLNGM TPEELNSYLHERSGKEGVFASFRLSGFGGSANVVVYACRPAHDEMAVDQCDKAGDFFVLGGPTEMP WRFYRAFHFDVTDSIDNIDKDRHGHYYVKAELFSVNGSALPNDLLPQPTISHRPARGHVDEAPAPS SDAHLAVRKDINHLTREEVYELRRAMERFQADTSVDGYQATVEYHGLPARCPFPEATNRFACCIHG MATFPHW

#### DOMAIN B

HRLFVTQVEDALIRRGSPIGVPYWDWTQPMAHLPGLADNATYRDPISGDSRHNPFHDVEVAFENGR TERHPDSRLFEQPLFGKHTRLFDSIVYAFEQEDFCDFEVQFEMTHNNIHAWIGGGGKYSMSSLHYT AFDPISYLHHSNTDRLWAIWQALQIRRNKPYKAHCAWSEERQPLKPFAFSSPLNNNEKTYENSVPT NVYDYEGVLGYTYDDLNFGGMDLGQLEEYIQRQRQRDRTFAGFFLSHIGTSANVEIIIDHGTLHTS VGTFAVLGGEKEMKWGFDRLYKYEITDELRQLNLRADDGFSISVKVTDVDGSELSSELIPSAAIIF ERSH

#### DOMAIN C

IDHQDPHQDTIIRKNVDNLTPEEINSLRRAMADLQSDKTAGGFQQIAAFHGEPKWCPSPDAEKKFS CCVHGMAVFPHWHRLLTVQGENALRKHGCLGALPYWDWTRPLSHLPDLVSQQNYTDAISTVEARNP WYSGHIDTVGVDTTRSVRQELYEAPGFGHYTGVAKQVLLALEQDDFCDFEVQFEIAHNFIHALVGG SEPYGMASLRYTTYDPIFYLHHSNTDRLWAIWQALQKYRGKPYNSANCAIASMRKPLQPFGLTDEI NPDDETRQHAVPFSVFDYKNNFNYEYDTLDFNGLSISQLDRELSRRKSHDRVFAGFLLHGIQQSAL VKFFVCKSDDDCDHYAGEFYILGDEAEMPWGYDRLYKYEITEQLNALDLHIGDRFFIRYEAFDLHG TSLGSNIFPKPSVIHDEGA

#### DOMAIN D

GHHQADEYDEVVTAASHIRKNLKDLSKGEVESLRSAFLQLQNDGVYENIAKFHGKPGLCDDNGRKV ACCVHGMPTFPQWHRLYVLQVENALLERGSAVSVPYWDWTETFTELPSLIAEATYFNSRQQTFDPN PFFRGKISFENAVTTRDPQPELYVNRYYYQNVMLAFEQDNYCDFEIQFEMVHNVLHAWLGGRATYS ISSLDYSAFDPVFFLHHANTDRLWAIWQELQRYRKKPYNEADCAINLMRKPLHPFDNSDLNHDPVT FKYSKPTDGFDYQNNFGYKYDNLEFNHFSIPRLEEIIRIRQRQDRVFAGFLLHNIGTSATVEIFVC VPTTSGEQNCENKAGTFAVLGGETEMAFHFDRLYRFDISETLRDLGIQLDSHDFDLSIKIQGVNGS YLDPHILPEPSLIFVPGSS

#### DOMAIN E

SFLRPDGHSDDILVRKEVNSLTTRETASLIHALKSMQEDHSPDGFQAIASFHALPPLCPSPSATHR YACCVHGMATFPQWHRLYTVQFQDALRRHGAAVGVPYWDWLRPQSHLPELVTMETYHDIWSNRDFP NPFYQANIEFEGENITTEREVIADKLFVKGGHVFDNWFFKQAILALEQENYCDFEIQFEILHNGVH TWVGGSRTHSIGHLHYASYDPLFYLHHSQTDRIWAIWQELQEQRGLSGDEAHCALEQMREPLKPFS FGAPYNLNQLTQDFSRPEDTFDYRKFGYEYDNLEFLGMSVAELDQYIIEHQENDRVFAGFLLSGFG GSASVNFQVCRADSTCQDAGYFTVLGGSAEMAWAFDRLYKYDITETLEKMHLRYDDDFTISVSLTA NNGTVLSSSLIPTPSVIFQRGH

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Fig. 7b

#### DOMAIN F

RDINTKSMSANRVRRELSDLSARDPSSLKSALRDLQEDDGPNGYQALAAFHGLPAGCHDSQGNEIA CCIHGMPTFPQWHRLYTLQLEMALRRHGSSVAIPYWDWTKPISELPSLFTSPEYYDPWHDAVVNNP FSKGFVKFANTYTVRDPQEMLFQLCEHGESILYEQTLLALEQTDYCDFEVQFEVLHNVIHYLVGGR QTYALSSLHYASYDPFFFIHHSFVDKMWVVWQALQKRRKLPYKRADCAVNLMTKPMRPFDSDMNQN PFTKMHAVPNTLYDYETLYYSYDNLEIGGRNLDQLQAEIDRSRSHDRVFAGFLLRGIGTSADVRFW ICRNENDCHRGGIIFILGGAKEMPWSFDRNFKFDITHVLEKAGISPEDVFDAEEPFYIKVEIHAVN KTMIPSSVIPAPTIIYSPGE

#### DOMAIN G

GRAADSAHSANIAGSGVRKDVTTLTVSETENLRQALQGVIDDTGPNGYQAIASFHGSPPMCEMNGR KVACCAHGMASFPHWHRLYVKQMEDALADHGSHIGIPYWDWTTAFTELPALVTDSENNPFHEGRID HLGVTTSRSPRDMLFNDPEQGSESFFYRQVLLALEQTDYCQFEVQFELTHNAIHSWTGGRSPYGMS TLEFTAYDPLFWLHHSNTDRIWAVWQALQKYRGLPYNEAHCEIQVLKQPLRPFNDDINHNPITKTN ARPIDSFDYERFNYQYDTLSFHGKSIPELNDLLEERKREERTFAAFLLRGIGCSADVVFDICRPNG DCVFAGTFAVLGGELEMPWSFDRLFRYDITRVMNQLHLQYDSDFSFRVKLVATNGTELSSDLLKSP TIEHEL

#### DOMAIN H

GAHRGPVEETEVTHQNTDGNAHFHRKEVDSLSLDEANNLKNALYKLQNDHSLTGYEAISGYHGYPN LCPEEGDDKYPCCVHGMAIFPHWHRLLTIQLERALEHNGALLGVPYWDWTKDLSSLPAFFSDSSNN NPYFKYHIAGVGHDTVREPTSLIYNQPQIHGYDYLYYLALTTLEENNYCDFEVQYEILHNAVHSWL GGSQKYSMSTLEYSAFDPVFMILHSGLDRLWIIWQELQKIRRKPYNFAKCAYHMMEEPLAPFSYPS INQDEFTRANSKPSTVFDSHKFGYHYDNLNVRGHSIQELNTIINDLRNTDRIYAGFVLSGIGTSAS VKIYLRTDDNDEEVGTFTVLGGEREMPWAYERVFKYDITEVADRLKLSYGDTFNFRLEITSYDGSV VNKSLPNPFIIYRPANHDYDVLVIPVGRNLHIPPKVVVKRGTRIEFHPVDDSVTRPVVDLGSYTAL FNCVVPPFTYRGFELNHVYSVKPGDYYVTGPTRDLCQNADVRIHIHVEDE

# Fig 8a

### Genomic sequence of the KLH1 gene

#### DOMAIN 1B

GGCCTACCGTACTGGGACTGGACTGAACCCATGACACACTTCCGGGTCTGGCAGGAAACAAAACT
TATGTGGATTCTCATGGTGCATCCCACACAAATCCTTTTCATAGTTCAGTGATTGCATTTGAAGAA
AATGCTCCCCACACCAAAAGACAAATAGATCAAAGACTCTTTTAAACCCGCTACCTTTGGACACCAC
ACAGACCTGTTCAACCAGATTTTGTATGCCTTTGAACAAGAAGATTACTGTGACTTTGAAGTCCAA
TTTGAGATTACCCATAACACGATTCACGCTTGGACAGGAGGAAGCGAACATTTCTCAATGTCGTC
CTACATTACACAGCTTTCGATCCTTTGTTTTACTTTCACCATTCTAACGTTGATCGTCTTTGGGCC
GTTTGGCAAGCCTTACAGATGAGACGGCATAAACCCTACAGGGCCCACTGCGCCATATCTCTGGAA
CATATGCATCTGAAACCATTCGCCTTTTCATCTCCCCTTAACAATAACGAAAAGACTCATGCCAAT
GCCATGCCAAACAAGATCTACGACTATGAAAATGTCCTCCATTACACATACGAAGATTTAACATTT
GGAGGCATCTCTCTGGAAAACATAGAAAAGATGATCCACGAAAACCAGCAAGAAGACAGAATATAT
GCCGGTTTTCTCCTGGCAGCATACGTACTTCAGCAAATGTTGATATCTTCATTAAAACTACCGAT
TCCGTGCAACATAAGGCTGGAACATTTGCAGTGCTCGGTGGAAGCAAGGAAATGAAGTGGGGATTT
GATCGCGTTTTCAAGTTTGACATCACGCACGTTTTGAAAGATCCACTGATCCACTGATGCGAT
TTCGAAGTTACTGTTGACATCACTGAAGTCGATGGAACTTAAACTTCCACTG

INTRON 1B/1C(SEQ ID NO:139)

#### DOMAIN 1C

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# Fig. 8b

INTRON 1C/1D (SEQ ID NO:140)

#### DOMAIN 1D

GTCACCATGAAGGCGAAGTATATCAAGCTGAAGTAACTTCTGCCAACCGTATTCGAAAAAACATTG AAAATCTGAGCCTTGGTGAACTCGAAAGTCTGAGAGCTGCCTTCCTGGAAAATTGAAAACGATGGAA CTTACGAATCAATAGCTAAATTCCATGGTAGCCCTGGTTTGTGCCAGTTAAATGGTAACCCCATCT CTTGTTGTGTCCATGGCATGCCAACTTTCCCTCACTGGCACAGACTGTACGTGGTTGTCGTTGAGA ATGCCCTCCTGAAAAAGGATCATCTGTAGCTGTTCCCTATTGGGACTGGACAAAACGAATCGAAC ATTTACCTCACCTGATTTCAGACGCCACTTACTACAATTCCAGGCAACATCACTATGAGACAAACC CATTCCATCATGGCAAAATCACACGAGAATGAAATCACTACTAGGGATCCCAAGGACAGCCTCT TCCATTCAGACTACTTTTACGAGCAGGTCCTTTACGCCTTGGAGCAGGATAACTTCTGTGATTTCG AGATTCAGTTGGAGATATTACACAATGCATTGCATTCTTTACTTGGTGGCAAAGGTAAATATTCCA TCTGGGCAATCTGGCAAGACCTTCAGAGGTTCCGAAAACGGCCATACCGAGAAGCGAATTGCGCTA TCCAATTGATGCACACGCCACTCCAGCCGTTTGATAAGAGCGACAACAATGACGAGGCAACGAAAA CGCATGCCACTCCACATGATGGTTTTGAATATCAAAACAGCTTTGGTTATGCTTACGATAATCTGG TATTCGCTGGCTTCCTCCTTCACAATATTGGAACATCTGCCGATGGCCATGTATTTGTATGTCTCC CAACTGGGGAACACGAAGGACTGCAGTCATGAGGCTGGTATGTTCTCCATCTTAGGCGGTCAAA CGGAGATGTCCTTTGTATTTGACAGACTTTACAAACTTGACATAACTAAAGCCTTGAAAAAAAGAACG GTGTGCACCTGCAAGGGGATTTCGATCTGGAAATTGAGATTACGGCTGTGAATGGATCTCATCTAG ACAGTCATGTCATCCACTCTCCCACTATACTGTTTGAGGCCGGAACAG

INTRON 1D/1E (SEQ ID NO:141)

#### DOMAIN 1E

## Fig. 8c

INTRON 1E/1F (SEQ ID NO:142)

DOMAIN 1F-1 (1st part of domain f)

INTRON 1F-1/1F-2 (SEQ ID NO:143)

DOMAIN 1F-2 (2nd part of domain f)

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# Fig. 8d

GTGGCATGCTGTATCCATGGAATGCCTACATTCCCCCACTGGCACAGACTCTACACCCTCCAATTT GAGCAAGCTCTAAGAAGACATGGCTCTAGTGTAGCAGTACCCTACTGGGACTGGACAAAGCCAATA CATAATATTCCACATCTGTTCACAGACAAAGAATACTACGATGTCTGGAGAAATAAAGTAATGCCA CTGTTCCACCTGACATCAACGGGTGAACACTCAGCGCTTCTGAATCAAGCTCTTTTGGCGCTGGAA CAGCACGACTACTGCGATTTTGCAGTCCAGTTTGAAGTCATGCACAACACAATCCATTACCTAGTG GGAGGACCTCAAGTCTATTCTTTGTCATCCCTTCATTATGCTTCATATGATCCGATCTTCTTCATA CACCACTCCTTTGTAGACAAGGTTTGGGCTGTCTGGCAGGCTCTTCAAGAAAAGAGAGGCCTTCCA TCAGACCGTGCTGACTGCGCTGTTAGTCTGATGACTCAGAACATGAGGCCTTTCCATTACGAAATT AACCATAACCAGTTCACCAAGAAACATGCAGTTCCAAATGATGTTTTCAAGTACGAACTCCTGGGT TACAGATACGACAATCTGGAAATCGGTGGCATGAATTTGCATGAAAATTGAAAAGGAAATCAAAGAC AAACAGCACCATGTGAGAGTGTTTGCAGGGTTCCTCCTTCACGGAATTAGAACCTCAGCTGATGTC CAATTCCAGATTTGTAAAACATCAGAAGATTGTCACCATGGAGGCCAAATCTTCGTTCTTGGGGGG ACTAAAGAGATGGCCTGGGCTTATAACCGTTTATTCAAGTACGATATTACCCATGCTCTTCATGAC GCACACATCACTCCAGAAGACGTATTCCATCCCTCTGAACCATTCTTCATCAAGGTGTCAGTGACA CTCGGTG

INTRON 1F-2/1G-1 (SEQ ID NO:144)

DOMAIN 1G-1 (1st part of domain g)

ACCATCACGAAGATCATCATTCTTCTATGGCTGGACATGGTGTCAGAAAGGAAATCAACACAC TTACCACTGCAGAGGTGGACAATCTCAAAGATGCCATGAGAGCCGTCATGGCAGACCACGGTCCAA ATGGATACCAGGCTATAGCAGCGTTCCATGGAAACCCACCAATGTGCCCTATGCCAGATGGAAAGA ATTACTCGTGTTGTACACATG

INTRON G1-1/1G-2 (SEQ ID NO:145)

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Fig. 8e

ATCTTTTCAAACAAGATTTTAGTATTTTGAAGACTTCTATGAATAAATTACACTTATGTGTTAGGT ATAGTTATCCTACTGTGGATAGTCTATATGAGAATCGTTGAAAGAATAATACAATTCTAATGGATT GCAACTTCTTTAACTTTTATTTGCAACTGCCACGTTTCGGTATACGTTCTTATGCCGTCATCAAGC ATACGAGTGTACATGTATGCCAAAACGCTGCAAATAAAAATTAAAGAAGTTGCAATCCATAAGAAT TTCAATGTTCTTTCATCATCACATCAACTTCTAAAAATGCCTATAAAACAATCAACAAACGTACAA TAGTACATTACCGGATCTCGCAGCATGACCACGTCGATATCTAAACAATATCACTATCCATTAATA GGATCAAGAGTAGGTACAGACATGTTCAGTTATAAATACTCTTCAAAAAAGTAGGGGAACTTGGAA TTTCAAGGTCAATAACAAACTAATGATAATAACAATTGGTCCCAAATAATAACAATTGGTCCCAAA CTAATTGTATCTTTACAAAGAAGAAATTGAGTGAACAATTCACCCGGTATTTTATTACCTAAACCG TTTCTCTTGCTGTTATGGTGCGTGAAAGAAGAAATGGGTAAGAAACGGAAATTGACATTTTTGCGT CGTCTACCTATGGTAATTTGATGCAGTCTGTCCCATTCTTCCACCAACGCCTGGACAAGTTCATCT AGCGTGGCTGGTGGCCTTTCACGTTGACGCACACGTCGGCCCAAGATGTCCCAGACATTTTCAATG GCCAGGGCTCATTGCTGGTCAGGGCATCCTATGGATATTGTGCCGTTGAAGGTGGTTATGTTGTTC ACATTGAAATTCCAAGTTCTCCTACTCTTTTTAAGAGGAGGTTCACAAAGTACGTTCTTTCATGTT GGTGAAGAGAATATCAAGGTCTTCTAAGGGATTGTGTCTTATAATATTTGATTTTAAGAAGTTTGA TATTATCTGCATCCTTCCCAAGAAATTGCAAATGTTCACACACTATTGCGTTTGATAATGTTTTTG GGGAAATAAACTGTCCAGGACTGCTAAATAGTAATTATTGCTACTTTTAG

DOMAIN 1G-2 (2nd part of domain g)

GCATGGCTACTTTCCCCCACTGGCACAGACTGTACACAAAACAGATGGAAGATGCCTTGACCGCCC ATGGTGCCAGAGTCGGCCTTCCTTACTGGGACGGACAACTGCCTTTACAGCTTTGCCAACTTTTG TCACAGATGAAGAGGACAATCCTTTCCATCAT

INTRON 1G-2/1G-3 (SEQ ID NO:146)

GTGAGTTCACGTAAGCCTACGAGATCAACATTACTCCTTAACAGCCACGGCATCATGTACCGATATAAGGACATGAGTCTGAAATAAACATGACTTGACACCGTTGTGGTCACAGTTTTGTTTCTCATTGGTGAACCTGTGAAACAACCTTTCAAACCAAAAGATGCCTATTAATATTGTTAATTCCCATGAATTAGG AGATACACACATTCTACTGTCATTT......AATAACCGCTTC CAGCATGAAAACACAATATGATTATCTCAATTCTACCATTACTAATTATAATTTTGACTGGCATTA TTTGACGACGCGTAAAACATCGCTGCTTTACAGACTGCACTGCGGTAACTGTGACGTTTTCATGACGTCACTACATTCTATTCAAAACATTTCCACAGAAGAGCGAGACCACGGCCGTGATGGGTTCTGGGCAGATGATTACCCAAGTATATATTTATAATAACTTGACTGCTTGCCTGAATAATGTTGACACATGAC AACGAATTTGTGATAGCGTAAGAAGCGTGAATACTGTGAATAGTGTGAGGGGTGTTTGCTGAGAGTTAACCACCGTTAATTGCAAAATTCCCGAATACTTGCATTTGCAGTCGAAGAAGAATTGCATTCTTACTCCTGTGAATGGACTCATTGTTATTTAGCAGCGGTTATTGAGGTTTTTGATCACCTCTAAATAGACAATCAGGATGCGGCAAACCGGAAAATTATAGCAGAATCTGTAATTCAAGATGGGCTTGCCTGTGAA AATATGCTGCGAGTTCAGTAACACTTTTCCCTTTCGATCATGGCCTGTTTTTGCTCTGAATCTGGTCTTTCAGAGGATCCCTGCTTTTTTAAAACTAAAGTCCTCCCAACTCACTTATATTTTATGTTTTTTAA 

DOMAIN 1G-3 (3rd part of domain g)

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## Fig. 9a

### Primary structure of the KLH1 protein

#### DOMAIN B

GLPYWDWTEPMTHIPGLAGNKTYVDSHGASHTNPFHSSVIAFEENAPHTKRQIDQRLFKPATFGHH TDLFNQILYAFEQEDYCDFEVQFEITHNTIHAWTGGSEHFSMSSLHYTAFDPLFYFHHSNVDRLWA VWQALQMRRHKPYRAHCAISLEHMHLKPFAFSSPLNNNEKTHANAMPNKIYDYENVLHYTYEDLTF GGISLENIEKMIHENQQEDRIYAGFLLAGIRTSANVDIFIKTTDSVQHKAGTFAVLGGSKEMKWGF DRVFKFDITHVLKDLDLTADGDFEVTVDITEVDGTKLASSLIPHASVIREHARGKLNR

#### DOMAIN C

VKFDKVPRSRLIRKNVDRLSPEEMNELRKALALLKEDKSAGGFQQLGAFHGEPKWCPSPEASKKFA CCVHGMSVFPHWHRLLTVQSENALRRHGYDGALPYWDWTSPLNHLPELADHEKYVDPEDGVEKHNP WFDGHIDTVDKTTTRSVQNKLFEQPEFGHYTSIAKQVLLALEQDNFCDFEIQYEIAHNYIHALVGG AQPYGMASLRYTAFDPLFYLHHSNTDRIWAIWQALQKYRGKPYNVANCAVTSMREPLQPFGLSANI NTDHVTKEHSVPFNVFDYKTNFNYEYDTLEFNGLSISQLNKKLEAIKSQDRFFAGFLLSGFKKSSL VKFNICTDSSNCHPAGEFYLLGDENEMPWAYDRVFKYDITEKLHDLKLHAEDHFYIDYEVFDLKPA SLGKDLFKQPSVIHEPRI

#### DOMAIN D

GHHEGEVYQAEVTSANRIRKNIENLSLGELESLRAAFLEIENDGTYESIAKFHGSPGLCQLNGNPI SCCVHGMPTFPHWHRLYVVVVENALLKKGSSVAVPYWDWTKRIEHLPHLISDATYYNSRQHHYETN PFHHGKITHENEITTRDPKDSLFHSDYFYEQVLYALEQDNFCDFEIQLEILHNALHSLLGGKGKYS MSNLDYAAFDPVFFLHHATTDRIWAIWQDLQRFRKRPYREANCAIQLMHTPLQPFDKSDNNDEATK THATPHDGFEYQNSFGYAYDNLELNHYSIPQLDHMLQERKRHDRVFAGFLLHNIGTSADGHVFVCL PTGEHTKDCSHEAGMFSILGGQTEMSFVFDRLYKLDITKALKKNGVHLQGDFDLEIEITAVNGSHL DSHVIHSPTILFEAG

#### DOMAIN E

TDSAHTDDGHTEPVMIRKDITQLDKRQQLSLVKALESMKADHSSDGFQAIASFHALPPLCPSPAAS KRFACCVHGMATFPQWHRLYTVQFQDSLRKHGAVVGLPYWDWTLPRSELPELLTVSTIHDPETGRD IPNPFIGSKIEFEGENVHTKRDINRDRLFQGSTKTHHNWFIEQALLALEQTNYCDFEVQFEIMHNG VHTWVGGKEPYGIGHLHYASYDPLFYIHHSQTDRIWAIWQSLQRFRGLSGSEANCAVNLMKTPLKP FSFGAPYNLNDHTHDFSKPEDTFDYQKFGYIYDTLEFAGWSIRGIDHIVRNRQEHSRVFAGFLLEG FGTSATVDFQVCRTAGDCEDAGYFTVLGGEKEMPWAFDRLYKYDITETLDKMNLRHDEIFQIEVTITSYDGTVLDSGLIPTPSIIYDPAH

#### DOMAIN F

HDISSHHLSLNKVRHDLSTLSERDIGSLKYALSSLQADTSADGFAAIASFHGLPAKCNDSHNNEVA CCIHGMPTFPHWHRLYTLQFEQALRRHGSSVAVPYWDWTKPIHNIPHLFTDKEYYDVWRNKVMPNP FARGYVPSHDTYTVRDVQEGLFHLTSTGEHSALLNQALLALEQHDYCDFAVQFEVMHNTIHYLVGG PQVYSLSSLHYASYDPIFFIHHSFVDKVWAVWQALQEKRGLPSDRADCAVSLMTQNMRPFHYEINH NQFTKKHAVPNDVFKYELLGYRYDNLEIGGMNLHEIEKEIKDKQHHVRVFAGFLLHGIRTSADVQF QICKTSEDCHHGGQIFVLGGTKEMAWAYNRLFKYDITHALHDAHITPEDVFHPSEPFFIKVSVTAV NGTVLPASILHAPTIIYEPGLG

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Fig. 9b

#### DOMAIN G

DHHEDHHSSSMAGHGVRKEINTLTTAEVDNLKDAMRAVMADHGPNGYQAIAAFHGNPPMCPMPDGK NYSCCTHGMATFPHWHRLYTKQMEDALTAHGARVGLPYWDGTTAFTALPTFVTDEEDNPFHHGHID YLGVDTTRSPRDKLFNDPERGSESFFYRQVLLALEQTD

## Fig. 10a

### Genomic sequence of the KLH2 gene

DOMAIN 2B

INTRON 2B/2C (SEQ ID NO:147)

GTATTTAAAAAAGTAATAAAACCATATTTTCGAATGCGCTTTATGAAATATCGTGTGACTGGTTCT TTAGTTTACATGGAGTGTAACAACATGCTCCATCAGTTGACATATACTGCTCACACAAAGTAAGGG ATATTTGATAATGATAACAAATATAATCAAAGCGGTTATACTATCAAGACTTATTCACATAATTAC AGGTGAAGGGAGGTGTGATCGTGTTCACTGATCAGGTTGAGGCCAGAGAAGTCCCAGTTTGAGTCT TGCAGAAGATGATGTTTAGGCATGGGGTCGAATCACCAAAATCACATGACTTCAATAACGGGTTGG ACCACCTCGAGCGACGATGCAAGCAGTAGAGCGTCTACGCATGCTCCTGATAAGGCGACCAATCTG TTCCTGGGGAATCAGTCGCCACTCCTCTTGTAGTGCCACGCTCATTTCTGCTACGGTCCTGGGTAC CTGCTATCGGGTCTTGATCCGTATCCCAAGGATGTCCCACACATGTTCAAGGTGAGAGGTCGGGGA ACATCGCTGGCCACGGTAAGGTCTGAATTTGATGCCGTTGAAAGTGAGCTCTGACAACCTGAGCAT GGTGAGCTCTGACGTTGTCGTCCTGAAAGATGAATCCAGCTCCATGACAGCGAGCAAAGGGCAGGA CGTGTTGGTCAATGCAGTTGTCTCTGCAGTACACCCTGTCACTCGCCACTCACAAGCGTGTAGAT CTGTACGACCAGTCATGGAGATCCCAGCCCACATCATAACGGACCCCTATCCATACCGATCATGAG CCACCATAGCAGCGTCTTGATGACGTTCTCCCTGTCGCCTCGACATCCTCACACGGCCAAAAGGAA CGTGGACTCGTCACTGAACATGACATTAGCCAACCTGGCACTTGTCCACCGCTGATGTTGGCGAGA CCATTCCAGTCGAGCTCTTCGGTGTCTGGCTTTCATCGATAACACGACGTAAGGTCTGCGGGCGTG CAAGACGCTCTATGCAGGCGATTTCGGATTGTCTGGGTGCTAACTCTGATCCCAGGTGCCTG AAGTTGATGCTGGATCTGTGTGGCATTGAGATGGCGATTCCTTAGGACTGTGGAGATGATGAATCG ATCTTGACTTATGGTGGTGACATTAGGACGTCGGGTTCGTGTCCTATCCTGCACTCTTCCAGTTGT TCGGTGACGCTCTGGTACCCGGCTGATTACTGACTGAGAATATCCATCTGCCGTGCGACATGAGCC TGTGTTGGCCCAGCCTGAAGCATTGCAATCGCCAGAGACGCTCTTCAAAAGTCATTCGACGCATGG TTTTCTGTTCACAAATGACAGCGTAAAACAGTTTTTGGTGCTTTTATGCTTCCCAAGAGCATGAAA AACACGTTCTATGGGTCGTGCACACCTTACATGACAAGTGTGAAAAGTGACTTGCACCCCCTTGTG TGTTCGGATGCACACTCTGTTTACGTACTGATGCGATTTGGCGTCTAAACATGTTTTGGCGTCTAA ACATGTTTTCCTGCATGATTCATATACTATTTTGTCATATTCCTGGCATCAAACCAAACTACAGTG AAATATATTTCAATATCCCCTACTTTGTGTGAGTAGTATAGATCACTGCAGACAACATATAGACAA TGCAGTTACACCGTCAACAATCCCAGTCATTAATTATGATGACACTTCCACACATAGTGTCAGTGA TTGTAATTCAACTGTACACACTTTTCCCGTGAACATTCAGGATCTATATGACTAAATATATAACAT TAGTATACGTGCAGTTTTGTATCGCTACGACATTGTTGTAACTCTTTGTTTAATCATTTAACAG

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## **Fig. 10b**

#### DOMAIN 2C

CTGATGCCAAAGACTTTGGCCATAGCAGAAAAATCAGGAAAGCCGTTGATTCTCTGACAGTCGAAG AACAAACTTCGTTGAGGCGAGCTATGGCAGATCTACAGGACGACAAAACATCAGGGGGTTTCCAGC AGATTGCAGCATTCCACGGAGAACCAAAATGGTGTCCAAGCCCCGAAGCGGAGAAAAAATTTGCAT GCTGTGTTCATGGAATGGCTGTTTTCCCTCACTGGCACAGATTGCTGACAGTTCAAGGAGAAAATG TTCCACATTTTGTTGCTGATCCTACTTACAATGATTCTGTTTCCAGCCTCGAAGAAGATAACCCAT GGTATCATGGTCACATAGATTCTGTTGGGCATGATACTACAAGAGCTGTGCGTGATGATCTTTATC AATCTCCTGGTTTCGGTCACTACACAGATATTGCAAAACAAGTCCTTCTGGCCTTTGAGCAGGACG ACGAACCATACAGTATGTCATCTTTGAGGTATACTACATACGATCCAATCTTCTTCTTGCACCGCT CCAATACAGACCGACTTTGGGCCATTTGGCAAGCTTTGCAAAAATACCGGGGGAAACCATACAACA CTGCAAACTGTGCCATTGCATCCATGAGAAAACCACTTCAGCCATTTGGTCTTGATAGTGTCATAA ATCCAGATGACGAAACTCGTGAACATTCGGTTCCTTTCCGAGTCTTCGACTACAAGAACAACTTCG ACTATGAGTATGAGAGCCTGGCATTTAATGGTCTGTCTATTGCCCAACTGGACCGAGAGTTGCAGA GAAGAAAGTCACATGACAGAGTCTTTGCAGGATTCCTTCTTCATGAAATTGGACAGTCTGCACTCG TGAAATTCTACGTTTGCAAACACAATGTATCTGACTGTGACCATTATGCTGGAGAATTCTACATTT TGGGAGATGAAGCTGAGATGCCTTGGAGGTATGACCGTGTGTACAAGTACGAGATAACACAGCAGC TGCACGATTTAGATCTACATGTTGGAGATAATTTCTTCCTTAAATATGAAGCCTTTGATCTGAATG GCGGAAGTCTTGGTGGAAGTATCTTTTCTCAGCCTTCGGTGATTTTCGAGCCAGCTGCAG

INTRON 2C/2D (SEQ ID NO:148)

#### DOMAIN 2D

GTTCACACCAGGCTGATGAATATCGTGAGGCAGTAACAAGCGCTAGCCACATAAGAAAAAATATCC GGGACCTCTCAGAGGGAGAAATTGAGAGCATCAGATCTGCTTTCCTCCAAATTCAAAAAGAGGGTA TATATGAAAACATTGCAAAGTTCCATGGAAAACCAGGACTTTGTGAACATGATGGACATCCTGTTG CTTGTTGTCCATGCCATGCCCACCTTTCCCCACTGGCACAGACTGTACGTTCTTCAGGTGGAGA ATGCGCTCTTAGAACGAGGGTCTGCAGTTGCTGTTCCTTACTGGGACTGGACCGAGAAAGCTGACT CTCTGCCATCATTAATCAATGATGCAACTTATTTCAATTCACGATCCCAGACCTTTGATCCTAATC CTTTCTTCAGGGGACATATTGCCTTCGAGAATGCTGTGACGTCCAGAGATCCTCAGCCAGAACTAT GGGACAATAAGGACTTCTACGAGAATGTCATGCTGGCTCTTGAGCAAGACAACTTCTGTGACTTTG AGATTCAGCTTGAGCTGATACACAACGCCCTTCATTCTAGACTTGGAGGAAGGGCTAAATACTCCC TTTCGTCTCTTGATTATACCGCATTTGATCCTGTATTTTTCCTTCACCATGCAAACGTTGACAGAA TCAACGAGATGCGTAAACCTCTTCAACCATTTAATAACCCAGAACTTAACAGTGATTCCATGACGC TTAAACACAACCTCCCACAAGACAGTTTTGATTATCAAAACCGCTTCAGGTACCAATATGATAACC TTCAATTTAACCACTTCAGCATACAAAAGCTAGACCAAACTATTCAGGCTAGAAAACAACACGACA GAGTTTTTGCTGGCTTTATTCTTCACAACATTGGGACATCTGCTGTTGTAGATATTTATATTTGCG TTGAACAAGGAGGAGAACAAAACTGCAAGACAAAGGCGGGTTCCTTCACGATTCTGGGGGGAGAAA CAGAAATGCCATTCCACTTTGACCGCTTGTACAAATTTGACATAACGTCTGCTCTGCATAAACTTG GTGTTCCCTTGGACGGACATGGATTCGACATCAAAGTTGACGTCAGAGCTGTCAATGGATCGCATC TTGATCAACACCTCAACGAACCGAGTCTGCTTTTTGTTCCTGGTGAACGTAAGAATATATTT ATG

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# Fig. 10c

INTRON 2D/2E (SEQ ID NO:149)

GTTATAAAGCAGTATATTCTCTTCAAAAAAGTAGGGGAACTTGGAATTTCAAGGTAAATAACATAA
CTACCTTCAACGGCACAATATCCATATGATGCCCTGGCCAGCAATGAGGCCTGATCTTTTCCCCAT
TAAAAATGTCTGGAACATCTTGGGCAAACGTGTGCGTCAACGTAAAACGCCACCAGTCACGCTAGA
TGAACTTGTCCAGGCGTTGGTGGAAGAATGGGACAGACTGCATCAATTACCATAAGTAGACTCATT
TGCAGCGAATCAGTCAGTGTTTGACCAATAACGGGGGCATTACGCACTACTGACGCAAAACAATGT
CAATTTCCGTTTCTTACCCATTCCTTCTTTCACGGACCATAACAGCAAGAGAAACTGNTTAGGTAA
TGAAATACCGGTGAATTATTGTTAACTGGATTCCTTCTTTGTAAAGATACAATTAGTTTGGGACCA
ATTATTATTATCATTAGTTTTGTTATTGACCTTGAAATTCGAAGTTCCTCTACATTTTTTAAGGAGT
TTATTTGATTGACAATGAAATGTAAGAAAAGAGCAAATCGTAAAAATACGTTAAAAATTATTCCTTA
AACATCAGTCTCTAACTTCAGTTTAAATTGCCAGTAACACGTGTTATATGATGTTTCCGTTTCTCT
TTGTTTTTTAGCATTCAACTTCAACTTGATATAACGTTTTACTGTTTTTAGATTCACATCAAACTGCAG

#### DOMAIN 2E

ATGGGCTTTCACAACATAATCTTGTGCGAAAAGAAGTAAGCTCTCTTACAACACTGGAGAAACATT TTTTGAGGAAAGCTCTCAAGAACATGCAAGCAGATGATTCTCCAGACGGATATCAAGCTATTGCTT CTTTCCACGCTTTGCCTCTTTTGTCCAAGTCCATCTGCTGCACATAGACACGCTTGTTGCCTCC ATGGTATGGCTACCTTCCCTCAGTGGCACAGACTCTACACAGTTCAGTTCGAAGATTCTTTGAAAC GACATGGTTCTATTGTCGGACTTCCATATTGGGATTGGCTGAAACCGCAGTCTGCACTCCCTGATT TGGTGACACAGGAGACATACGAGCACCTGTTTTCACACAAAACCTTCCCAAATCCGTTCCTCAAGG CAAATATAGAATTTGAGGGAGAGGGGGTAACAACAGAGAGGGATGTTGATGCTGAACACCTCTTTG CAAAAGGAAATCTGGTTTACAACAACTGGTTTTGCAATCAGGCACTATATGCACTAGAACAAGAAA CAAAGACCCATTCAATAGGTCATCTTCATTACGCATCATACGATCCACTGTTCTATATCCACCATT CGCAGACAGATCGCATTTGGGCTATCTGGCAAGCTCTCCAGGAGCACAGAGGTCTTTCAGGGAAGG AAGCACACTGCGCCCTGGAGCAAATGAAAGACCCTCTCAAACCTTTCAGCTTTGGAAGTCCCTATA ATTTGAACAAACGCACTCAAGAGTTCTCCAAGCCTGAAGACACATTTGATTATCACCGATTCGGGT ATGAGTATGATTCCCTCGAATTTGTTGGCATGTCTGTTTCAAGTTTACATAACTATATAAAACAAC AACAGGAAGCTGATAGAGTCTTCGCAGGATTCCTTCTTAAAGGATTTGGACAATCAGCATCCGTAT CGTTTGATATCTGCAGACCAGACCAGAGTTGCCAAGAAGCTGGATACTTCTCAGTTCTCGGTGGAA GTTCAGAAATGCCGTGGCAGTTTGACAGGCTTTACAAGTACGACATTACAAAAACGTTGAAAGACA TGAAACTGCGATACGATGACACATTTACCATCAAGGTTCACATAAAGGATATAGCTGGAGCTGAGT TGGACAGCGATCTGATTCCAACTCCTTCTGTTCTCCTTGAAGAAGGAAAGC

INTRON 2E/2F (SEQ ID NO:150)

DOMAIN 2F-1 (1st part of domain f)

ATGGGATCAATGTACGTCACGTTGGTCGTAATCGGATTCGTATGGAACTATCTGAACTCACCGAGA GAGATCTCGCCAGCCTGAAATCTGCAATGAGGTCTCTACAAGCTGACGATGGGGTGAACGGTTATC AAGCCATTGCATCACTCACGGTCTCCCGGCTTCTTGTCATGATGATGAGGGACATGAG

# Fig. 10d

INTRON 2F (SEO ID NO:151)

DOMAIN 2F-2 (2nd part of domain f)

ATTGCCTGTTGTATCCACGGAATGCCAGTATTCCCACACTGGCACAGGCTTTACACCCTGCAAATG GACATGGCTCTGTTATCTCACGGATCTGCTGTTGCTATTCCATACTGGGACTGGACCAAACCTATC AGCAAACTGCCTGATCTCTTCACCAGCCCTGAATATTACGATCCTTGGAGGGGATGCAGTTGTCAAT AATCCATTTGCTAAAGGCTACATTAAATCCGAGGACGCTTACACGGTTAGGGATCCTCAGGACATT TTGTACCACTTGCAGGACGAAACGGGAACATCTGTTTTGTTAGATCAAACTCTTTTAGCCTTAGAG CAGACAGATTTCTGTGATTTTTGAGGTTCAATTTGAGGTCGTCCATAATGCTATTCACTACTTGGTG GGTGGTCGACAAGTTTATGCTCTTTCTTCAACACTATGCTTCATATGACCCAGCCTTCTTTATT CATCACTCCTTTGTTGACAAAATATGGGCAGTCTGGCAAGCTCTGCAAAAGAAGAGAAAGCGTCCC TATCATAAAGCGGATTGTGCTCTTAACATGATGACCAAACCAATGCGACCATTTGCACACGATTTC AATCACAATGGATTCACAAAAATGCACGCAGTCCCCAACACTCTATTTGACTTTCAGGACCTTTTC TACACGTATGACAACTTAGAAATTGCTGGCATGAATGTTAATCAGTTGGAAGCGGAAATCAACCGG CGAAAAAGCCAAACAAGAGTCTTTGCCGGGTTCCTTCTACATGGCATTGGAAGATCAGCTGATGTA CGATTTTGGATTTGCAAGACAGCTGACGACTGCCACGCATCTGGCATGATCTTTATCTTAGGAGGT TCTAAAGAGATGCACTGGGCCTATGACAGGAACTTTAAATACGACATCACCCAAGCTTTGAAGGCT CAGTCCATACACCCTGAAGATGTGTTTGACACTGATGCTCCTTTCTTCATTAAAGTGGAGGTCCAT GGTGTAAACAAGACTGCTCTCCCATCTTCAGCTATCCCAGCACCTACTATAATCTACTCAGCTGGT GAAG

INTRON 2F-2/2G (SEQ ID NO:152)

DOMAIN 2G-1 (1st part of domain q)

INTRON 2G-1/2G-2 (SEQ ID NO:153)

## Fig. 10e

TCAACAATTGTTTGAGTTTTAATGCAAGAAAATTATCAGGAGTAGCGTGCAAAAATGACTGGAAGG CATGGTGTACTTCTGTGTGTACATACAAGTGGGTAATGCCTTATTGAACTCGTAATCACTCGTTTC AG

DOMAIN 2G-2 (2nd part of domain g)

INTRON 2G-2/2G-3 (SEQ ID NO:154)

DOMAIN 2G-3 (3rd part of domain g)

INTRON 2G/2H (SEQ ID NO:155)

GTATGTTTTGAGATCCACATAATCTTCTACCCTGTCTCATTTCTAATGCTCTTCAATACACAATTT ATATAGCCTTTGAGCTTCAGATGTATTACGGACAGGCATTACAGTATACATGTAATATGGTTTTCT GCTATTTGCAAAAATTGTGTCCTATCTCTGTTCAGATCATCATGGCGGTGACACCTAG

DOMAIN 2H (SEQ ID NO:159)

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## Fig. 11a

### Primary structure of the KLH2 protein

#### DOMAIN B

GLPYWDWTMPMSHLPELATSETYLDPVTGETKNNPFHHAQVAFENGVTSRNPDAKLFMKPTYGDHT YLFDSMIYAFEQEDFCDFEVQYELTHNAIHAWVGGSEKYSMSSLHYTAFDPIFYLHHSNVDRLWAI WQALQIRRGKSYKAHCASSQEREPLKPFAFSSPLNNNEKTYHNSVPTNVYDYVGVLHYRYDDLQFG GMTMSELEEYIHKQTQHDRTFAGFFLSYIGTSASVDIFINREGHDKYKVGSFVVLGGSKEMKWGFD RMYKYEITEALKTLNVAVDDGFSITVEITDVDGSPPSADLIPPPAIIFDVVR

#### DOMAIN C

ADAKDFGHSRKIRKAVDSLTVEEQTSLRRAMADLQDDKTSGGFQQIAAFHGEPKWCPSPEAEKKFA CCVHGMAVFPHWHRLLTVQGENALRKHGFTGGLPYWDWTRPMSALPHFVADPTYNDSVSSLEEDNP WYHGHIDSVGHDTTRAVRDDLYQSPGFGHYTDIAKQVLLAFEQDDFCDFEVQFEIAHNFIHALVGG NEPYSMSSLRYTTYDPIFFLHRSNTDRLWAIWQALQKYRGKPYNTANCAIASMRKPLQPFGLDSVI NPDDETREHSVPFRVFDYKNNFDYEYESLAFNGLSIAQLDRELQRRKSHDRVFAGFLLHEIGQSAL VKFYVCKHNVSDCDHYAGEFYILGDEAEMPWRYDRVYKYEITQQLHDLDLHVGDNFFLKYEAFDLN GGSLGGSIFSQPSVIFEPAA

#### DOMAIN D

GSHQADEYREAVTSASHIRKNIRDLSEGEIESIRSAFLQIQKEGIYENIAKFHGKPGLCEHDGHPV ACCVHGMPTFPHWHRLYVLQVENALLERGSAVAVPYWDWTEKADSLPSLINDATYFNSRSQTFDPN PFFRGHIAFENAVTSRDPQPELWDNKDFYENVMLALEQDNFCDFEIQLELIHNALHSRLGGRAKYS LSSLDYTAFDPVFFLHHANVDRIWAIWQDLQRYRKKPYNEADCAVNEMRKPLQPFNNPELNSDSMT LKHNLPQDSFDYQNRFRYQYDNLQFNHFSIQKLDQTIQARKQHDRVFAGFILHNIGTSAVVDIYIC VEQGGEQNCKTKAGSFTILGGETEMPFHFDRLYKFDITSALHKLGVPLDGHGFDIKVDVRAVNGSH LDQHILNEPSLLFVPGERKNIYY

#### DOMAIN E

DGLSQHNLVRKEVSSLTTLEKHFLRKALKNMQADDSPDGYQAIASFHALPPLCPSPSAAHRHACCL HGMATFPQWHRLYTVQFEDSLKRHGSIVGLPYWDWLKPQSALPDLVTQETYEHLFSHKTFPNPFLK ANIEFEGEGVTTERDVDAEHLFAKGNLVYNNWFCNQALYALEQENYCDFEIQFEILHNGIHSWVGG SKTHSIGHLHYASYDPLFYIHHSQTDRIWAIWQALQEHRGLSGKEAHCALEQMKDPLKPFSFGSPY NLNKRTQEFSKPEDTFDYHRFGYEYDSLEFVGMSVSSLHNYIKQQQEADRVFAGFLLKGFGQSASV SFDICRPDQSCQEAGYFSVLGGSSEMPWQFDRLYKYDITKTLKDMKLRYDDTFTIKVHIKDIAGAE LDSDLIPTPSVLLEEGK

#### DOMAIN F

HGINVRHVGRNRIRMELSELTERDLASLKSAMRSLQADDGVNGYQAIASFHGLPASCHDDEGHEIA CCIHGMPVFPHWHRLYTLQMDMALLSHGSAVAIPYWDWTKPISKLPDLFTSPEYYDPWRDAVVNNP FAKGYIKSEDAYTVRDPQDILYHLQDETGTSVLLDQTLLALEQTDFCDFEVQFEVVHNAIHYLVGG RQVYALSSQHYASYDPAFFIHHSFVDKIWAVWQALQKKRKRPYHKADCALNMMTKPMRPFAHDFNH NGFTKMHAVPNTLFDFQDLFYTYDNLEIAGMNVNQLEAEINRRKSQTRVFAGFLLHGIGRSADVRF WICKTADDCHASGMIFILGGSKEMHWAYDRNFKYDITQALKAQSIHPEDVFDTDAPFFIKVEVHGV NKTALPSSAIPAPTIIYSAGE

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# Fig. 11b

#### DOMAIN G

DHIAGSGVRKDVTSLTASEIENLRHALQSVMDDDGPNGFQAIAAYHGSPPMCHMPDGRDVACCTHG MASFPHWHRLFVKQMEDALAAHGAHIGIPYWDWTSAFSHLPALVTDHEHNPFHHGHIAHRNVDTSR SPRDMLFNDPEHGSESFFYRQVLLALEQTDFCQFEVQFEITHNAIHSWTGGHTPYGMSSLEYTAYD PLFYLHHSNTDRIWAIWQALQKYRGFQYNAAHCDIQVLKQPLKPFSESRNPNPVTRANSRAVDSFD YERLNYQYDTLTFHGHSISELDAMLQERKKEERTFAAFLLHGFGASADVSFDVCTPDGHCAFAGTF AVLGGELEMPWSFERLFRYDITKVLKQMNLHYDSEFHFELKIVGTDGTELPSDRIKSPTIEHHGG

#### DOMAIN H (SEQ ID NO:158)

GHDHSERHDGFFRKEVGSLSLDEANDLKNALYKLQNDQGPNGYESIAGYHGYPFLCPEHGEDQYACCVHGMPVFPHWHRLHTIQFERALKEHGSHLGLPYWDW